

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 03:56:09 ; Search time 198 Seconds
(without alignments)
1276.973 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

Sequence: 1 MVQRLLVSRLLRHRKAQLL.....AIYFATQVVFQKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	553	2 AAW69385	AAW69385 Prostate
2	2861	100.0	553	2 AAW71869	AAW71869 Amino aci
3	2861	100.0	553	3 AAY82002	AAY82002 Human Imm
4	2861	100.0	553	3 AAB28527	AAB28527 Protein e
5	2861	100.0	553	3 ABG94411	ABG94411 Human pro
6	2861	100.0	553	4 AAM01117	AAM01117 Human pro
7	2861	100.0	553	4 AAU69763	AAU69763 Human pro
8	2861	100.0	553	4 AAB74800	AAB74800 Prostate
9	2861	100.0	553	4 AAG99002	AAG99002 Human pro
10	2861	100.0	553	4 AAG62150	AAG62150 Human P50
11	2861	100.0	553	4 ABU71653	ABU71653 Prostate
12	2861	100.0	553	4 AAU04961	AAU04961 Human pro
13	2861	100.0	553	5 AAU10324	AAU10324 Human PRO
14	2861	100.0	553	5 ABB95222	ABB95222 Human L1-
15	2861	100.0	553	5 AAU82843	AAU82843 Human bre
16	2861	100.0	553	5 ABB61900	ABB61900 Prostate
17	2861	100.0	553	5 ABB76665	ABB76665 Prostate
18	2861	100.0	553	5 ABB77575	ABB77575 Human mas
19	2861	100.0	553	6 ABR54334	ABR54334 Prostate
20	2861	100.0	553	7 ADB13563	ADB13563 Human pro
21	2861	100.0	553	7 ADG25979	ADG25979 Human pro
22	2861	100.0	553	7 ADK68076	ADK68076 Novel NOV
23	2861	100.0	553	7 ADN39584	ADN39584 Cancer/an

24	2861	100.0	553	7 ADN39230	Adn39230 Cancer/an
25	2861	100.0	553	8 ADH10469	Adh10469 Human P50
26	2861	100.0	553	8 ADG74153	Adg74153 Human pro
27	2861	100.0	553	8 ADR49065	Adr49065 Human NOV
28	2861	100.0	553	9 AEA00147	Aea00147 Human TAT
29	2861	100.0	553	9 AEA00667	Aea00667 Human TAT
30	2861	100.0	553	10 AEF66260	Aef66260 Human pro
31	2861	100.0	560	8 ADR65983	Adr65983 Human pro
32	2861	100.0	560	8 ADR66881	Adr66881 Human pro
33	2861	100.0	694	8 ADH10472	Adh10472 Codon-opt
34	2861	100.0	1079	4 AAB74830	Aab74830 Prostate
35	2861	100.0	1079	4 ABU71860	Abu71860 Prostate
36	2856	99.8	553	10 AEF66853	Aef66853 Human pro
37	2798	97.8	553	8 ADG74151	Adg74151 Monkey pr
38	2773.5	96.9	694	8 ADH10474	Adh10474 Codon-opt
39	2704	94.5	685	8 ADH10457	Adh10457 Human P50
40	2619	91.5	553	8 ADG74149	Adg74149 Rat prost
41	2610	91.2	644	8 ADH10471	Adh10471 P501S-CPC
42	2610	91.2	644	8 ADH10470	Adh10470 CPC- P501
43	2610	91.2	652	8 ADH10467	Adh10467 CPC-P501S
44	2610	91.2	652	8 ADH10453	Adh10453 CPC- P501
45	2610	91.2	671	8 ADH10459	Adh10459 CPC- P501

ALIGNMENTS

RESULT 1

AAW69385
ID AAW69385 standard; protein; 553 AA.

AC AAW69385;

XX

XX

DT 25-MAR-2003 (revised)

DT 08-DEC-1998 (first entry)

XX

DE Prostate tumour specific gene clone L1-12 protein.

XX

KW Prostate tumour specific gene; human; prostate cancer; detection;

KW therapy.

XX

OS Homo sapiens.

XX

PN WO9837418-A2.

XX

PD 27-AUG-1998.

XX

PF 25-FEB-1998; 98WO-US003690.

XX

PR 25-FEB-1997; 97US-00806596.

PR 01-AUG-1997; 97US-00904809.

PR 09-FEB-1998; 98US-00020747.

XX

(CORI-) CORIXA CORP.

 XX | Xu J, | Dillon DC; || XX | WPI; | 1998-480805/41. |
XX	N-PSDB;	AAV58586.
XX	Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers.	
XX	Example 1; Page 87-89; 141pp; English.	
XX	This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.	

DE Human immunogenic prostate tumour protein sequence SEQ ID NO:113.
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine.
XX OS Homo sapiens.
XX WO200004149-A2.
XX 27-JAN-2000.
XX 14-JUL-1999; 99WO-US015838.
XX 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX (CORI-) CORIXA CORP.
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 3; Page 138-139; 263pp; English.
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
XX the present invention
XX Sequence 553 AA;
SQ
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLRHRKQAQLLLNLLTFGLVCLAAAGTYYVPPILLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWVSRLRHRKQAQLLLNLLTFGLVCLAAAGTYYVPPILLLEVGVEEKFMTWVLGIG 60
QY 61 PVILGLVCPVLGSGSDHNRGRRPFTWALSGLTLLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVILGLVCPVLGSGSDHNRGRRPFTWALSGLTLLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLLDFCQCVCTPLEALLSDLPDPCRQAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVLLDFCQCVCTPLEALLSDLPDPCRQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTALAPYLGTQBECLFGLLTILFTCVAAATLLVABEALGPTPEAGLSAPSLSPH 240
DB 181 IDWDTALAPYLGTQBECLFGLLTILFTCVAAATLLVABEALGPTPEAGLSAPSLSPH 240
QY 241 CCPCBARAFNLGALLPRLHOLCCMPRTLRLFVAELCSNMALMTFTLFTDFVGEGL 300
DB 241 CCPCBARAFNLGALLPRLHOLCCMPRTLRLFVAELCSNMALMTFTLFTDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360

DB 301 YQGVPRABPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDLSAPLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYFATQ 540
DB 481 RVVPGRGICLDLAILDLSAPLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAYFATQ 540
QY 541 VVFDKSLAKYSA 553
DB 541 VVFDKSLAKYSA 553
RESULT 4
AAB28527
ID AAB28527 standard; protein; 553 AA.
XX
AC AAB28527;
XX
DT 07-FEB-2001 (first entry)
XX
DE Protein encoded by human breast tumour cDNA clone P501S.
XX Human; breast tumour antigen; cytostatic; immunotherapy; breast cancer;
KW vaccine.
XX Homo sapiens.
OS
XX WO200061756-A2.
PN
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009688.
PF
XX 09-APR-1999; 99US-00288950.
PR
XX 02-JUL-1999; 99US-00346327.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC;
XX
XX WPI; 2000-638568/61.
DR
XX N-PSDB; AAC79473.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
PT cancer.
XX
PS Claim 2; Page 92-93; 95pp; English.
XX
XX The present sequence is encoded by a cDNA sequence which was isolated
CC from a breast tumour cDNA library. It is provided in a specification
CC relating to compounds for immunotherapy and diagnosis of breast cancer.
CC Breast tumour antigens and the polynucleotides that encode them may be
CC used in the production of a pharmaceutical composition to be used in the
CC treatment of breast cancer. Proliferated T cells and incubated antigen
CC presenting cells are also required. The polypeptides and polynucleotides
CC may also be used to produce a vaccine
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLRHRKQAQLLLNLLTFGLVCLAAAGTYYVPPILLLEVGVEEKFMTWVLGIG 60

	DB	1	MVQRLWSRLLRHKQAQLLWNLLTFGLEVCYLAAGITVPPLLELVGVGEFKFMTWVLGIG	60
	QY	61	PVLGLVCVPLLGSADHWRCRGRRRPFTWALSGLILLSFLI PRAGMLAGLLCCDPDRPL	120
	DB	61	PVLGLVCVPLLGSADHWRCRGRRRPFTWALSGLILLSFLI PRAGMLAGLLCCDPDRPL	120
	QY	121	ELALLILGVGLDFCGQVCFPLEALLSD.LFRDPDHCROAYSIVYAFMISLGCGCLGYLLPA	180
	DB	121	ELALLILGVGLDFCGQVCFPLEALL.SDLFRDPDHCROAYSIVYAFMISLGCGCLGYLLPA	180
	QY	181	IDWOTSALAPYLGTQEBSCLGLTLTFLTCTCAATLVAEEAALGPTEPAEGLSAPSLSPH	240
	DB	181	IDWOTSALAPYLGTQEBSCLFGLLTLFLTCTCAATLVAEEAALGPTEPAEGLSAPSLSPH	240
	QY	241	CCPCRARLAFNLLGALLPRLHLQLCMRPTRLRLFWAEICSMNALMTFTFLTYDFVGEGGL	300
	DB	241	CCPCRARLAFNLLGALLPRLHLQLCMRPTRLRLFWAEICSMNALMTFTFLTYDFVGEGGL	300
	QY	301	YGCVPRABPGTEARRHYDEGVRMGSLGFLOCAISLVFSLVMDRLVQRFGTRAVYLASA	360
	DB	301	YGCVPRABPGTEARRHYDEGVRMGSLGFLFOCAISLVFSLVMDRLVQRFGTRAVYLASA	360
	QY	361	APPVAAGATCLSHSVAVVTASAAULTGFTFSALQILPYTLASLYHREKVFLPKYRGDTGG	420
	DB	361	APPVAAGATCLSHSVAVVTASAAULTGFTFSALQILPYTLASLYHREKVFLPKYRGDTGG	420
	QY	421	ASSEDLSMTSFLLPGPKCAPFPNGHVHGAGSGLLPPBPALCGASACDVSVRVVVGBPTBA	480
	DB	421	ASSEDLSMTSFLLPGPKCAPFPNGHVHGAGSGLLPPBPALCGASACDVSVRVVVGBPTBA	480
	J	481	RVPVGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATO	540
	QY	481	RVPVGRGICLDLAILDSAFLLSQVAPSLFMGSI VQLSQSVTAYMVSAAGLGLVAIFYATO	540
	QY	541	VVFVDKSDIAKYGA	553
	DB	541	VVFVDKSDIAKYGA	553

RESULT 5
ABG94411
ID ARG94411 standard: protein: 553 AA.

XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX
PS Example 1; Page 59-61; 10lpp; English.
XX
XX The present invention relates to a new polypeptide comprising an
CC immunogenic portion of a prostate protein. The invention is useful for
CC inhibiting the development of prostate cancer in a patient. The invention
CC is also useful as markers for diagnosing prostate cancer and for
CC monitoring diseases progression in patients. The present amino acid
CC sequence represents a human prostate tumour protein
XX
SO sequence 553 AA;

RESULT 6
AAM01117
ID AAM01117 standard: protein; 553 AA.

```
OS Homo sapiens.
XX WO2001151633-A2.
XX
XX PD 19-JUL-2001.
XX
XX PF 16-JAN-2001; 2001WO-US001574.
XX
XX PR 14-JAN-2000; 2000US-00483672.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.
XX
XX Claim 2; Page 267-268; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytotstatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate
XX volume. AAH93357 to AAH93944 and AAM0115 to AAM01318 represent
XX polynucleotide and amino acid sequences used in the exemplification of
XX the present invention
XX
XX Sequence 553 AA;
XX
XX *Query Match 100.0%; Score 2861; DB 4; Length 553;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-268;
XX Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MVQRLWVSRLLHRKQAQILLNLLTFGLVCLAGITYVPPLLLLEVGVEEKPMTWVLGIG 60
DB 1 MVQRLWVSRLLHRKQAQILLNLLTFGLVCLAGITYVPPLLLLEVGVEEKPMTWVLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRGRRRPFIIWALSGLISLFLI PRAGWLAGLLCPDPRPL 120
DB 61 PVLGLVCVPLLGASDHWGRGRRRPFIIWALSGLISLFLI PRAGWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDPCQVCFTPLEALLSDLPDPDHCQQAQSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILVGLLDPCQVCFTPLEALLSDLPDPDHCQQAQSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSPH 240
DB 181 IDWDTSAAPYLGTQECLFGLLTILFLTCVAATLLVAEEAALGTEPAEGLSAPLSPH 240
QY 241 CCPCRARLAFRLNGLALLPRLHQLCCRMPTLRLFAELCSNMALMTFTLFTYDFVGEGL 300
DB 241 CCPCRARLAFRLNGLALLPRLHQLCCRMPTLRLFAELCSNMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYASVA 360
QY 361 APPVAAGATCLSHSVAVVTASALTGFTFSALQILPYTLASLYHREKQVFLPKYGDGTGG 420
DB 361 APPVAAGATCLSHSVAVVTASALTGFTFSALQILPYTLASLYHREKQVFLPKYGDGTGG 420
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QY 421 ASSEDSLMTSFLPGPKGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVOLSQSVTAYMYSAAGLGLVAFYATQ 540
DB 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVOLSQSVTAYMYSAAGLGLVAFYATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553
XX
XX RESULT 7
XX ID AAU69763 standard; protein; 553 AA.
XX AC AAU69763;
XX
XX DT 30-JAN-2002 (first entry)
XX
XX DE Human prostate cDNA encoded protein #3.
XX
XX KW Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
XX
XX OS Homo sapiens.
XX
XX PN WO2001173032-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-US009919.
XX
XX PR 27-MAR-2000; 2000US-00536857.
XX PR 09-MAY-2000; 2000US-00568100.
XX PR 12-MAY-2000; 2000US-00570737.
XX PR 13-JUN-2000; 2000US-00593793.
XX PR 27-JUN-2000; 2000US-00605783.
XX PR 09-AUG-2000; 2000US-00636215.
XX PR 29-AUG-2000; 2000US-00651236.
XX PR 06-SEP-2000; 2000US-00657279.
XX PR 02-OCT-2000; 2000US-00679426.
XX PR 10-OCT-2000; 2000US-00685166.
XX PR 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX N-PSDB; AAS63557.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 2; Page 269-270; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polypeptide of the invention
XX
XX Sequence 553 AA;
```

Query Match	100.0%;	Score 2661;	DB 4;	Length 553;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-268;			
Matches 553;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1	1	1	1	1	1
1	1	1	1	1	1
61	1	1	1	1	1
61	1	1	1	1	1
121	1	1	1	1	1
121	1	1	1	1	1
181	1	1	1	1	1
181	1	1	1	1	1
241	1	1	1	1	1
241	1	1	1	1	1
301	1	1	1	1	1
301	1	1	1	1	1
361	1	1	1	1	1
361	1	1	1	1	1
421	1	1	1	1	1
421	1	1	1	1	1
481	1	1	1	1	1
481	1	1	1	1	1
541	1	1	1	1	1
541	1	1	1	1	1
RESULT 8					
AB74800					
AB74800 standard; protein; 553 AA.					
IC X					
14-JUN-2001 (first entry)					
Prostate tumour antigen predicted amino acid sequence for L1-12.					
Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;					
prostate cancer; immunogenic; cytostatic; vaccine.					
Homo sapiens.					
WO200125272-A2.					
12-APR-2001.					
04-OCT-2000; 2000WO-US027464.					
04-OCT-1999; 99US-0157455P.					
(CORI-) CORIXA CORP.					
Xu J, Steiky YAW, Reed SG, Cheever MA;					

AC AAG99002;
XX 25-SEP-2001 (first entry)
XX Human prostate-specific amino acid sequence L1-12/P501S.
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA.
XX Homo sapiens.
OS
XX WO2001134802-A2.
XX 17-MAY-2001.
XX 09-NOV-2000; 2000WO-US030904.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX Claim 3; Page 167-168; 325pp; English.
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLHRKQAQLLLNLLTFGLVCLVLAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60
Db 1 MVORLWVSRLLHRKQAQLLLNLLTFGLVCLVLAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60
QY 61 PVGLVGVPLIGSADHWGRYGRRRPFTWALSGLTLLSLFLI PRAGWLAGLLCPDPRPL 120
Db 61 PVGLVGVPLIGSADHWGRYGRRRPFTWALSGLTLLSLFLI PRAGWLAGLLCPDPRPL 120
QY 121 ELALITLGVGLDFGQVCFPTLEALLSLDFDPDHCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALITLGVGLDFGQVCFPTLEALLSLDFDPDHCQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTOBECFLGLLTLIFLCVAATLLVAEEAALGPTEPAEGLSAPLSHP 240
Db 181 IDWTSALAPYLGTOBECFLGLLTLIFLCVAATLLVAEEAALGPTEPAEGLSAPLSHP 240
QY 241 CCPCARLARFNLGALLPRHLQCCMPRTLRFLVAELCSNMALMTFTLFTDFVGEGL 300
Db 241 CCPCARLARFNLGALLPRHLQCCMPRTLRFLVAELCSNMALMTFTLFTDFVGEGL 300

QY 301 YQGVPRABPGTEARRHYDEGVMSGLGLFLQCAISLVFSLVMDRLVQREGTRAVYLSVA 360
Db 301 YQGVPRABPGTEARRHYDEGVMSGLGLFLQCAISLVFSLVMDRLVQREGTRAVYLSVA 360
QY 361 APPVAAAGATCLSHSVAVVTASAAALTGFTFSALQIILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAAGATCLSHSVAVVTASAAALTGFTFSALQIILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVVGPEPTA 480
Db 421 ASSEDSLMTSFLPGPKGAPPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVVGPEPTA 480
QY 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFMGSIIVLSQSVTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFMGSIIVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 10
AAG62150
ID AAG62150 standard; protein; 553 AA.
XX AC AAG62150;
XX 06-JUL-2001 (first entry)
XX Human P501S inventive antigen SEQ ID NO: 333.
DE Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.
XX Homo sapiens.
OS WO200125273-A2.
XX 12-APR-2001.
XX 04-OCT-2000; 2000WO-US027465.
XX 04-OCT-1999; 99US-0157459P.
XX (CORI-) CORIXA CORP.
XX Skeiky YAW, Xu J, Cheever MA, Reed SG;
PI WPI; 2001-328324/34.
XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WTI.
XX Disclosure; Page 212-213; 228pp; English.
XX The present invention describes compositions comprising peptides derived
CC from the wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a polypeptide described in the exemplification of the invention
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLHRKQAQLLLNLLTFGLVCLVLAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60

PA	(STOL//) STOLK J A.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSMTSFLPGPKPGAPFNGHVGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSMTSFLPGPKPGAPFNGHVGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFPMGSIIVOLQSQSVTAYMVSAAAGLGLVAIFYFATQ 540
Db 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFPMGSIIVOLQSQSVTAYMVSAAAGLGLVAIFYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 12
AAU04961
ID AAU04961 standard; protein; 553 AA.
AC AAU04961;
XX
XX 24-OCT-2001 (first entry)
XX
DE Human prostate tumour protein L1-12.
KW Human; prostate tumour protein; prostate cancer.
XX
XX Homo sapiens.
XX
XX US6262245-B1.
XX
XX 17-JUL-2001.
XX
XX 25-FEB-1998; 98US-00030607.
XX
XX 25-FEB-1997; 97US-00806099.
XX
XX 01-AUG-1997; 97US-00904804.
XX
XX 09-FEB-1998; 98US-00020956.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC;
XX
XX WPI; 2001-440862/47.
XX
XX N-PSDB; AAS10108.
XX
XX Novel polynucleotide encoding polypeptide comprising a portion of
XX prostate tumor protein useful for inhibiting development of prostate
XX cancer or for treating prostate cancer in a patient.
XX
XX Example 1; Col 125-127; 105pp; English.
XX
XX The sequence is a partial prostate tumour protein, encoded by a prostate
XX tumour specific cDNA. The DNA is useful for inhibiting the development of
XX prostate cancer or for treating prostate cancer in a patient
XX
XX Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-266;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLRHRKAQLLLNLLTFGLBVCVLAAGTIVVPLLLEVGVEKEKMTWVLGIG 60
Db 1 MVQRLWVSRLLRHRKAQLLLNLLTFGLBVCVLAAGTIVVPLLLEVGVEKEKMTWVLGIG 60
QY 61 PVILGVCVPLLSASDHWGRYGRRRPFTIWSLGLLSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVILGVCVPLLSASDHWGRYGRRRPFTIWSLGLLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLIDFCQGVCFPLEALLSDLPDPDHCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVLIDFCQGVCFPLEALLSDLPDPDHCQAYSVYAFMISLGGCLGYLLPA 180
```

```
QY 181 IDWDTSAAPYLGTQEECLFGLITLIFLTCAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWDTSAAPYLGTQEECLFGLITLIFLTCAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNGLGALLPRLHQLCCRMPTLRLRFLVAELCSMMALMTFTLFTYDFVGBGL 300
Db 241 CCPCRARLAFRNGLGALLPRLHQLCCRMPTLRLRFLVAELCSMMALMTFTLFTYDFVGBGL 300
QY 301 YQGVPRABPGTEARHRYDEGVRMGSGLGLPLOCALSLVFSLVMDRLVORFGTRAVYLASVA 360
Db 301 YQGVPRABPGTEARHRYDEGVRMGSGLGLPLOCALSLVFSLVMDRLVORFGTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSMTSFLPGPKPGAPFNGHVGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSMTSFLPGPKPGAPFNGHVGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFPMGSIIVOLQSQSVTAYMVSAAAGLGLVAIFYFATQ 540
Db 481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFPMGSIIVOLQSQSVTAYMVSAAAGLGLVAIFYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 13
AAU10324
ID AAU10324 standard; protein; 553 AA.
XX
XX AC AAU10324;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human PROST 03.
XX
XX Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
XX cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX WO200181577-A2.
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013323.
XX
XX 27-APR-2000; 2000US-0200065P.
XX
XX 20-APR-2001; 2001US-00838785.
XX
XX (SCHD ) SCHERING AG.
XX
XX Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
XX Van Heuit PT, Wu J;
XX
XX WPI; 2002-041404/05.
XX
XX N-PSDB; AAS14962.
XX
XX Novel PROST 03 polypeptides and polynucleotides useful in research,
XX diagnosis and therapeutic applications, particularly for use in cancer
XX therapeutics.
XX
XX Claim 14; Fig 2; 77pp; English.
XX
XX The invention relates to an isolated PROST 03 polypeptide (I) and to the
XX polynucleotide (II) encoding PROST 03. Fragments of (I) were used to
XX generate antibodies (III) to PROST 03. (III) is useful for selectively
XX destroying a cell expressing (I), and for treating a disease-state
XX associated with expression of PROST 03 in a human patient. (III) is
```

CC useful for diagnosing metastasis associated with (I), in a subject. (I)
CC is also useful for diagnosing and treating diseases of cell proliferation
CC such as prostate cancers. (I) is also useful for generating antibodies to
CC PROST 03. (III) is useful in detecting the levels of PROST 03
CC polypeptides in cells and tissues, and in targeting drugs to primary and
CC metastatic tumours. (I) is also useful for stimulating immune response to
CC PROST 03 containing cells. (II) is useful in diagnostic assays for
CC detecting the levels of polynucleotides encoding PROST 03 in cells and
CC tissues. (II) is useful as DNA probes, as targets for antisense and
CC ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents the
CC amino acid sequence of human PROST 03
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLMVSRLRRKKAQLLVNLTFTGLEVCLAAAGITYVPPLLLEVGVBEKFTMWLIG 60
Db 1 MVQRLMVSRLRRKKAQLLVNLTFTGLEVCLAAAGITYVPPLLLEVGVBEKFTMWLIG 60

QY 61 PVGLGVCVPLGSGSDHWRGRRPFTWALSIGLILSLFLIPRAGWLAGLCCPDPRL 120
Db 61 PVGLGVCVPLGSGSDHWRGRRPFTWALSIGLILSLFLIPRAGWLAGLCCPDPRL 120

QY 121 ELALLIGVGLLDFCGQVCFPTLEALLSDLFRDPDHCRAQSVYAFPMISLGGCLGYLLPA 180
Db 121 ELALLIGVGLLDFCGQVCFPTLEALLSDLFRDPDHCRAQSVYAFPMISLGGCLGYLLPA 180

QY 181 IDWDTALAPYLGTQECFLGGLTLFLTCVAATLLVABEALGPTPEAGLSAPLSLSPH 240
Db 181 IDWDTALAPYLGTQECFLGGLTLFLTCVAATLLVABEALGPTPEAGLSAPLSLSPH 240

QY 241 CCPCRLARLAFNLCALLPRHLQCCRMPTLRLFVAELCSWMLMTFTLFYDFVGEGL 300
Db 241 CCPCRLARLAFNLCALLPRHLQCCRMPTLRLFVAELCSWMLMTFTLFYDFVGEGL 300

QY 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQREGTRAVVLSVA 360
Db 301 YQGVPAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQREGTRAVVLSVA 360

QY 361 APFVAAGATCLSHSAVAVTASAAALGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGC 420
Db 361 APFVAAGATCLSHSAVAVTASAAALGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGC 420

QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480

QY 481 RVVPGRGICLDIALDSAFELSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAFYATQ 540
Db 481 RVVPGRGICLDIALDSAFELSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAFYATQ 540

QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 14
ABB95222
ID ABB95222 standard; protein; 553 AA.
XX
AC ABB95222;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human L1-12 protein SEQ ID NO 113.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy.

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Homo sapiens.
OS
XX US2002022248-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 12-JAN-2001; 2001US-00759143.
PF
XX
XX 25-FEB-1997; 97US-00806099.
PR
XX 01-AUG-1997; 97US-00904804.
PR
XX 10-FEB-1998; 98US-00020956.
PR
XX 25-FEB-1998; 98US-00030607.
PR
XX 14-JUL-1998; 98US-00115453.
PR
XX 23-SEP-1998; 98US-00159812.
PR
XX 15-JAN-1999; 99US-00232149.
PR
XX 09-APR-1999; 99US-00288946.
PR
XX 13-JUL-1999; 99US-00352616.
PR
XX 12-NOV-1999; 99US-00439313.
PR
XX 18-NOV-1999; 99US-00443686.
PR
XX 14-JAN-2000; 2000US-00483672.
PR
XX 27-MAR-2000; 2000US-00536857.
PR
XX 09-MAY-2000; 2000US-00568100.
PR
XX 12-MAY-2000; 2000US-00570737.
PR
XX 13-JUN-2000; 2000US-00593793.
PR
XX 27-JUN-2000; 2000US-00605783.
PR
XX 10-AUG-2000; 2000US-00636215.
PR
XX 29-AUG-2000; 2000US-00651236.
PR
XX 06-SEP-2000; 2000US-00657279.
PR
XX 02-OCT-2000; 2000US-00679426.
PR
XX 10-OCT-2000; 2000US-00685166.
XX
XX(XUJJ/) XU J.
PA
XX(DILL/) DILLON D C.
PA
XX(MITC/) MITCHAM J L.
PA
XX(HARL/) HARLOCKER S L.
PA
XX(JIAN/) JIANG Y.
PA
XX(KALO/) KALOS M D.
PA
XX(FANG/) FANGER G R.
PA
XX(RETT/) RETTER M W.
PA
XX(STOL/) STOLK J A.
PA
XX(DAYC/) DAY C H.
PA
XX(VEDV/) VEDVICK T S.
PA
XX(CART/) CARTER D.
PA
XX(LISX/) LI S X.
PA
XX(WANG/) WANG A.
PA
XX(SKEI/) SKEIKY Y A W.
PA
XX(HEPL/) HEPLER W T.
PA
XX(HEND/) HENDERSON R A.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 113; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC protein described in the invention
XX
SQ Sequence 553 AA;

QY 1 MVQRLWVSRLRHRKAQALLVNLTLFTGLEVCIAAGITVVPPLLLLEGVVEKEKFTMTVLGIG 60
Db 1 MVQRLWVSRLRHRKAQALLVNLTLFTGLEVCIAAGITVVPPLLLLEGVVEKEKFTMTVLGIG 60
QY 61 PVILGLVCPVLLGSADHWGRYGRRRPFIWALSGLILLSLFLIPRAGMWLAGLLCPDPRPL 120
Db 61 PVILGLVCPVLLGSADHWGRYGRRRPFIWALSGLILLSLFLIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
Db 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
QY 241 CCPCARLAFRNLGALLPRHLQCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCARLAFRNLGALLPRHLQCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIVOLQSQVTAAYMVSAAAGLGLVAYFATQ 540
Db 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIVOLQSQVTAAYMVSAAAGLGLVAYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 15

AAU82643
ID AAU82643 standard; peptide; 553 AA.
XX AC AAU82643;
XX DT 23-APR-2002 (first entry)
XX DE Human breast tumour polypeptide clone #3.
XX KW Human; breast tumour polypeptide; breast cancer; cytostatic;
KW immunostimulant.
XX OS Homo sapiens.
XX PN WO200198339-A2.
XX PD 27-DEC-2001.
XX PF 12-JUN-2001; 2001WO-US019032.
XX PR 22-JUN-2000; 2000US-00602877.
PR 12-OCT-2000; 2000US-00687507.
PR 06-FEB-2001; 2001US-00778381.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX WPI; 2002-147792/19.
DR N-PSDB; ABK29012.
XX

PT Polynucleotides encoding breast tumor polypeptides, useful for treating breast cancer or stimulating an immune response.
PT Claim 2; Page 144-145; 150pp; English.
XX The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention
XX Sequence 553 AA;
SQ

Query Match 100.0%; Score 2861; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1e-268; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;
QY 1 MVQRLWVSRLRHRKAQALLVNLTLFTGLEVCIAAGITVVPPLLLLEGVVEKEKFTMTVLGIG 60
Db 1 MVQRLWVSRLRHRKAQALLVNLTLFTGLEVCIAAGITVVPPLLLLEGVVEKEKFTMTVLGIG 60
QY 61 PVILGLVCPVLLGSADHWGRYGRRRPFIWALSGLILLSLFLIPRAGMWLAGLLCPDPRPL 120
Db 61 PVILGLVCPVLLGSADHWGRYGRRRPFIWALSGLILLSLFLIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILGVGLLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLLDFCGOVCFPLEALLSDLPDPDHCROAVSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
Db 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAATLLVAEEAALGTEPAEGLSAPLSLSPH 240
QY 241 CCPCARLAFRNLGALLPRHLQCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCARLAFRNLGALLPRHLQCCRMPTLRRLFVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGVWMSGLFLQCAISLVFSLVMDRLVQRFGRTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIVOLQSQVTAAYMVSAAAGLGLVAYFATQ 540
Db 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIVOLQSQVTAAYMVSAAAGLGLVAYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

Search completed: May 27, 2006, 03:59:38
Job time : 203 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2006, 04:05:04 ; Search time 50 seconds
(without alignments)
968,089 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHRAQLLL.....AIYFATQVVDKSLAKYSA 553

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2861	100.0	553	2	US-09-020-956-113 Sequence 113, App
2	2861	100.0	553	2	US-09-030-607-113 Sequence 113, App
3	2861	100.0	553	2	US-09-439-313-113 Sequence 113, App
4	2861	100.0	553	2	US-09-352-616A-113 Sequence 113, App
5	2861	100.0	553	2	US-09-602-877A-101 Sequence 101, App
6	2861	100.0	553	2	US-09-232-149A-113 Sequence 113, App
7	2861	100.0	553	2	US-09-159-812-113 Sequence 113, App
8	2861	100.0	553	2	US-09-636-215-113 Sequence 113, App
9	2861	100.0	553	2	US-09-685-166A-113 Sequence 113, App
10	2861	100.0	553	2	US-09-115-453-113 Sequence 113, App
11	2861	100.0	553	2	US-09-688-489-113 Sequence 113, App
12	2861	100.0	553	2	US-09-679-426-113 Sequence 113, App
13	2861	100.0	553	2	US-09-759-143-113 Sequence 113, App
14	2861	100.0	553	2	US-09-651-236-113 Sequence 113, App
15	2861	100.0	553	2	US-09-030-606-113 Sequence 113, App
16	2861	100.0	553	2	US-09-657-279-113 Sequence 113, App
17	2861	100.0	553	2	US-10-012-896-113 Sequence 113, App
18	2861	100.0	553	3	US-09-116-134-113 Sequence 113, App
19	2861	100.0	553	3	US-10-144-678A-113 Sequence 113, App
20	1517	53.0	305	3	US-10-144-678A-1029 Sequence 1028, Ap
21	1417.5	49.5	371	2	US-09-636-215-708 Sequence 708, App
22	1417.5	49.5	371	2	US-09-685-166A-708 Sequence 708, App
23	1417.5	49.5	371	2	US-09-679-426-708 Sequence 708, App
24	1417.5	49.5	371	2	US-09-759-143-708 Sequence 708, App
25	1417.5	49.5	371	2	US-09-651-236-708 Sequence 708, App
26	1417.5	49.5	371	2	US-09-657-279-708 Sequence 708, App

27	1417.5	49.5	371	2	US-10-012-896-708	Sequence 708, App
28	1417.5	49.5	371	3	US-10-144-678A-708	Sequence 708, App
29	1403.5	49.1	400	2	US-09-636-215-852	Sequence 852, App
30	1403.5	49.1	400	2	US-09-685-166A-852	Sequence 852, App
31	1403.5	49.1	400	2	US-09-679-426-852	Sequence 852, App
32	1403.5	49.1	400	2	US-09-759-143-852	Sequence 852, App
33	1403.5	49.1	400	2	US-09-651-236-852	Sequence 852, App
34	1403.5	49.1	400	2	US-09-657-279-852	Sequence 852, App
35	1403.5	49.1	400	2	US-10-012-896-852	Sequence 852, App
36	1403.5	49.1	400	3	US-10-144-678A-852	Sequence 36, Appl
37	1287	45.0	255	2	US-09-071-710-36	Sequence 36, Appl
38	1287	45.0	255	2	US-09-525-397-36	Sequence 1028, Ap
39	1197	41.8	246	3	US-10-144-678A-1028	Sequence 1011, Ap
40	947	33.1	355	3	US-10-012-896-1011	Sequence 1011, Ap
41	947	33.1	355	3	US-10-144-678A-1011	Sequence 571, App
42	452	15.8	84	2	US-09-439-313-571	Sequence 706, App
43	426	14.9	123	2	US-09-636-215-706	Sequence 706, App
44	426	14.9	123	2	US-09-685-166A-706	Sequence 706, App
45	426	14.9	123	2	US-09-679-426-706	Sequence 706, App

ALIGNMENTS

RESULT 1
US-09-020-956-113
; Sequence 113, Application US/09020956
; Patent No. 6261582
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLLRHRAQLLLNLLFTGLEVCLAAAGITYVPPLLLEVGVEKEKMTWVLGIG 60
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Db	1	MVQRLWVSRLLRHRKAQLLLVNLLTFGLVCLAAAGTYVPPLLLEVGVEEKFMVTLVIG	60
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Db	61	PVLGLVCPVLLGSADHWRGRRPFIWALSGLILLSFLIPRAGWLAGLLCPDRPL	120
Qy	121	ELALLILVGLLDFCGQVCFTEALLSDLPDPDCHCRQAYSVAFMISLGGCIGYLLPA	180
Db	121	ELALLILVGLLDFCGQVCFTEALLSDLPDPDCHCRQAYSVAFMISLGGCIGYLLPA	180
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Db	181	IDWTSALAPYLGTOBECLFGLLTFLTCVAATLLVAEEAALGTEPAEGLSAPLSPH	240
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Db	241	CCPCRLARLAFNLGALLPRHLQCCRMPTLRRLFVAELCSNMALMTFTLFTDFVGEGL	300
Qy	301	YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA	360
Db	301	YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA	360
Qy	361	AFVVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Db	361	AFVVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Qy	421	ASSEDSLMTSFLPGPKPGAPPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEPA	480
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Qy	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIFYATQ	540
Db	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIFYATQ	540
Qy	541	VVFDKSDLAKYSA	553
Db	541	VVFDKSDLAKYSA	553
RESULT 2			
US-09-030-607-113			
; Sequence 113, Application US/09030607			
; Patent No. 6262245			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO			
; NUMBER OF SEQUENCES: 224			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SEED and BERRY LLP			
; STREET: 6300 Columbia Center, 701 Fifth Avenue			
; CITY: Seattle			
; STATE: WA			
; COUNTRY: USA			
; ZIP: 98104			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/030,607			
; FILING DATE: 25-FEB-1998			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Maki, David J.			
; REGISTRATION NUMBER: 31,392			
; REFERENCE/DOCKET NUMBER: 210121.427C3			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (206) 622-4900			
; TELEFAX: (206) 682-6031			
; INFORMATION FOR SEQ ID NO: 113:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 553 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; ORIGINAL SOURCE:			
; ORGANISM: Homo sapiens			
US-09-030-607-113			
Query Match			
100.0%; Score 2861; DB 2; Length 553;			
Best Local Similarity 100.0%; Pred. No. 1.5e-270;			
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MVQRLWVSRLLRHRKAQLLLVNLLTFGLVCLAAAGTYVPPLLLEVGVEEKFMVTLVIG	60
Qy	61	PVLGLVCPVLLGSADHWRGRRPFIWALSGLILLSFLIPRAGWLAGLLCPDRPL	120
Db	61	PVLGLVCPVLLGSADHWRGRRPFIWALSGLILLSFLIPRAGWLAGLLCPDRPL	120
Qy	121	ELALLILVGLLDFCGQVCFTEALLSDLPDPDCHCRQAYSVAFMISLGGCIGYLLPA	180
Db	121	ELALLILVGLLDFCGQVCFTEALLSDLPDPDCHCRQAYSVAFMISLGGCIGYLLPA	180
Qy	181	IDWTSALAPYLGTOBECLFGLLTFLTCVAATLLVAEEAALGTEPAEGLSAPLSPH	240
Db	181	IDWTSALAPYLGTOBECLFGLLTFLTCVAATLLVAEEAALGTEPAEGLSAPLSPH	240
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Db	241	CCPCRLARLAFNLGALLPRHLQCCRMPTLRRLFVAELCSNMALMTFTLFTDFVGEGL	300
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Db	301	YQGVPRAEPTGEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFTRAVYLASVA	360
Qy	361	AFVVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Db	361	AFVVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Qy	421	ASSEDSLMTSFLPGPKPGAPPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEPA	480
Db	421	ASSEDSLMTSFLPGPKPGAPPFNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEPA	480
Qy	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIFYATQ	540
Db	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIFYATQ	540
Qy	541	VVFDKSDLAKYSA	553
Db	541	VVFDKSDLAKYSA	553
RESULT 3			
US-09-439-313-113			
; Sequence 113, Application US/09439313			
; Patent No. 6329505			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang Yuqi			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Kalos, Michael			
; APPLICANT: Fanger, Gary			
; APPLICANT: Retter, Mark			
; APPLICANT: Solk, John			
; APPLICANT: Day, Craig			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C9			

; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-439-313-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVORLWVSRLLRHKAQALLVNLTFGLVCLAAAGITYVPPILLLEVGVEKFTMWLGIG 60
DB 1 MVORLWVSRLLRHKAQALLVNLTFGLVCLAAAGITYVPPILLLEVGVEKFTMWLGIG 60
QY 61 PVGLVCVPLLGASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLLGASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDFOGQVCFPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILVGLLDFOGQVCFPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTEPAEGLSAPLSPH 240
DB 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTEPAEGLSAPLSPH 240
QY 241 CCPCRARLAFRLNIGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYTDVFVGEGL 300
DB 241 CCPCRARLAFRLNIGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYTDVFVGEGL 300
QY 301 YGVVPAEPTGTRRHHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRTGTRAVYLA 360
DB 301 YGVVPAEPTGTRRHHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRTGTRAVYLA 360
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DB 361 APVVAAGATCLSHVAVVTASALTCFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVAAGLGLVAYIFATQ 540
DB 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVAAGLGLVAYIFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 4
US-09-352-616A-113
; Sequence 113, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113

; LENGTH: 553
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-352-616A-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVORLWVSRLLRHKAQALLVNLTFGLVCLAAAGITYVPPILLLEVGVEKFTMWLGIG 60
DB 1 MVORLWVSRLLRHKAQALLVNLTFGLVCLAAAGITYVPPILLLEVGVEKFTMWLGIG 60
QY 61 PVGLVCVPLLGASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLLGASDHWRGRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILVGLLDFOGQVCFPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILVGLLDFOGQVCFPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTEPAEGLSAPLSPH 240
DB 181 IDWTSALAPYLGTOECLFGLTLFLTCVAATLLVAEEAALGPTEPAEGLSAPLSPH 240
QY 241 CCPCRARLAFRLNIGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYTDVFVGEGL 300
DB 241 CCPCRARLAFRLNIGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYTDVFVGEGL 300
QY 301 YGVVPAEPTGTRRHHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRTGTRAVYLA 360
DB 301 YGVVPAEPTGTRRHHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRTGTRAVYLA 360
QY 361 APVVAAGATCLSHVAVVTASALTCFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APVVAAGATCLSHVAVVTASALTCFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVAAGLGLVAYIFATQ 540
DB 481 RVVPGRGICLDLALDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVAAGLGLVAYIFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 5
US-09-602-877A-101
; Sequence 101, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-602-877A-101

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;

	Matches	553;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
Qy	1	MVORLWVSRLLRHRAQ	1LLVNLITFGLEVCL	AAGITVYPPLLELVGVEE	KMTVMVLGIG	60				
Db	1	MVORLWVSRLLRHRAQ	1LLVNLITFGLEVCL	AAGITVYPPLLELVGVEE	KMTVMVLGIG	60				
Qy	61	PVLGLVVCVPLLGASD	HWGRYGRRRPFIWALS	LGILLSLFIPRAGWLAGLL	CPDRPRL	120				
Db	61	PVLGLVVCVPLLGASD	HWGRYGRRRPFIWALS	LGILLSLFIPRAGWLAGLL	CPDRPRL	120				
Qy	121	ELALLILGVGLLDFCGQ	VCTPPEALLSDLFRPD	HCRQAYSVYATFMSI	SGGLGVLLPA	180				
Db	121	ELALLILGVGLLDFCGQ	VCTPPEALLSDLFRPD	HCRQAYSVYATFMSI	SGGLGVLLPA	180				
Qy	181	IDWDTSAALPYLGTE	ECFLGLTLIFLTCVA	ATLVAEEAALGPTE	PAEGLSAPLSPH	240				
Db	181	IDWDTSAALPYLGTE	ECFLGLTLIFLTCVA	ATLVAEEAALGPTE	PAEGLSAPLSPH	240				
Qy	241	CCPCBARLAFNRLG	ALLPRLHQLCCMRP	TRLRLFVAELCSNMAL	TFTFLFYTDFVGEGL	300				
Db	241	CCPCBARLAFNRLG	ALLPRLHQLCCMRP	TRLRLFVAELCSNMAL	TFTFLFYTDFVGEGL	300				
Qy	301	YOGVPRAEPGTEARR	HYDEGVYRMSGLFL	QCAISLVFSLVMDRL	VQFCTRAVYLASA	360				
Db	301	YOGVPRAEPGTEARR	HYDEGVYRMSGLFL	QCAISLVFSLVMDRL	VQFCTRAVYLASA	360				
Qy	361	APPVAAAGATCLSHS	VAVVTASAALTGTFT	SALQILPYTLASLVH	RKQVFLPKYRGDTGG	420				
Db	361	APPVAAAGATCLSHS	VAVVTASAALTGTFT	SALQILPYTLASLVH	RKQVFLPKYRGDTGG	420				
Qy	421	ASSDSLMTSFLPGPK	APCPNGHVGAGSGLL	PPPALCGASACDVS	VVVVVGPEPTEA	480				
Db	421	ASSDSLMTSFLPGPK	APCPNGHVGAGSGLL	PPPALCGASACDVS	VVVVVGPEPTEA	480				
Qy	481	RVPVPGRGICLDLAI	LDSAFLLSQVAPSLF	MGSIYQLSQSVTAY	VMWSAAGLGLVAI	540				
Db	481	RVPVPGRGICLDLAI	LDSAFLLSQVAPSLF	MGSIYQLSQSVTAY	VMWSAAGLGLVAI	540				
Qy	541	VVFVDSKSDLAKYSA	553							
Db	541	VVFVDSKSDLAKYSA	553							

```

RESULT 6
US-09-232-149A-113
; Sequence 113, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-149A-113

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RESULT 7
US-09-159-812-113
; Sequence 113, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159.812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-159-812-113

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	Query Match	100.0%; Score 2861; DB 2;	Length 553;
	Best Local Similarity	100.0%; Prod.No.1.5e-270;	
	Matches 553; Conservative	0; Mismatches 0; Indels	0; Gaps 0
QY	1 MVQLRWVSRLLRHRAQALLNLTFFGLEVCCLAAGITYVPPLLEVGVEEKFMTMVLGIG	60	
Dd	1 MVQLRWVSRLLRHRAQALLNLTFFGLEVCCLAAGITYVPPLLEVGVEEKFMTMVLGIG	60	
OV	61 PVLGHCVCPPDGLGSADHWGRGVRRRPDIWLSGIILLFLFIPTRACGLWAGLCCDPDRPL	120	

Db 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLARFNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
Db 241 CCPCRARLARFNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
QY 301 YQGVPAEPTGTEARRHYDEGVRMGSGLGLFLOCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
Db 301 YQGVPAEPTGTEARRHYDEGVRMGSGLGLFLOCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 8

US-09-636-215-113
; Sequence 113, Application US/09636215
; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-636-215-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLLHRKQAQLLVNLLTFGLVCLAAAGITYVPPLLVGVBEKEKMTWVLGIG 60
Db 1 MVQRLWVSRLLHRKQAQLLVNLLTFGLVCLAAAGITYVPPLLVGVBEKEKMTWVLGIG 60
QY 61 PVGLGVCVPLLSASDHWRGRRPFTIWSLGLLSLFLIPRAGMWLAGLLCPDPRPL 120

Db 61 PVGLGVCVPLLSASDHWRGRRPFTIWSLGLLSLFLIPRAGMWLAGLLCPDPRPL 120
QY 121 ELALLILGVLGDLDFGCVCFTEPLEALLSDLFDPDPCRQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVLGDLDFGCVCFTEPLEALLSDLFDPDPCRQAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
Db 181 IDWDTSAAPYLGTOECLFGLLTILFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLARFNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
Db 241 CCPCRARLARFNIGALLPRHLQOLCCRMPTLRRLFVAELCSWMALMTFTFLFYTDFFVGEGL 300
QY 301 YQGVPAEPTGTEARRHYDEGVRMGSGLGLFLOCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
Db 301 YQGVPAEPTGTEARRHYDEGVRMGSGLGLFLOCAISLVFSLVMDRLVQREGTTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIYFATQ 540
Db 481 RVVPGRGICLDLAIDLSDAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 9

US-09-685-166A-113
; Sequence 113, Application US/09685166A
; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-685-166A-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
Db 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
Db 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYTDFVGEGL 300
Db 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYTDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRFGRVAVLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRFGRVAVLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVAVIYFATQ 540
Db 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVAVIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 10
US-09-115-453-113
; Sequence 113, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-115-453-113
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
Db 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
Db 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240

QY 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYTDFVGEGL 300
Db 241 CCPCRARLAFRNLGALLPRLHQLCCRMPTLRLRFLVAELCSWMALMTFTLYTDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRFGRVAVLASVA 360
Db 301 YQGVPRABPGTEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQRFGRVAVLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVAVIYFATQ 540
Db 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVAVIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 11
US-09-688-489-113
; Sequence 113, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-688-489-113
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
Db 1 MVQRLWVSRLRRHKAQLLLVNLTLFGLVCLAAAGTIVVPPLLLEVGVEEKEFTMWLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
Db 61 PVLGLVCVPLLGASDHWGRYGRRRPFTWALSIGLISLFLIPRAGWLAGLLCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFTEALSLDFRDPDHCROQAYSVYAFMISLGCGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTILFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240

Db 181 IDWTSALAPYLGTQBECLFGLLTLLFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
QY 241 CCPCRARLAFRNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCRARLAFRNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPAEPGTARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
Db 301 YQGVPAEPGTARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASALTGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASALTGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 12
US-09-679-426-113
; Sequence 113, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-426-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No.1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLVWSRLRRKKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKMTWVLGIG 60
Db 1 MVQRLVWSRLRRKKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKMTWVLGIG 60
QY 61 PVGLVCVPLLGASDHWGRYGRRRPFTWALSGLILLSFLIPRAGWLAGLLCPDPREL 120
Db 61 PVGLVCVPLLGASDHWGRYGRRRPFTWALSGLILLSFLIPRAGWLAGLLCPDPREL 120

QY 121 ELALLILGVGLLDFCGQVCFTTLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLLDFCGQVCFTTLEALLSDLFRDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQBECLFGLLTLLFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
Db 181 IDWTSALAPYLGTQBECLFGLLTLLFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH 240
QY 241 CCPCRARLAFRNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
Db 241 CCPCRARLAFRNIGALLPRHLQCCCRMPRTLRLFLVAELCSWMALMTFTLFTYDFVGEGL 300
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Db 301 YQGVPAEPGTARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
QY 361 APPVAAGATCLSHSVAVVTASALTGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASALTGTFTSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 13
US-09-759-143-113
; Sequence 113, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-113

Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No.1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLVCLAGITVVPPLLLLEVGVVEEKFTMTVLGIG 60
Db 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLVCLAGITVVPPLLLLEVGVVEEKFTMTVLGIG 60
QY 61 PVLGLVCVPLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCCDPRPL 120
Db 61 PVLGLVCVPLGASDHWGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLCCDPRPL 120
QY 121 ELALLILGVGLDFCGQVCFPTLEALLSDLFRDPDHCROAYSVAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVGLDFCGQVCFPTLEALLSDLFRDPDHCROAYSVAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
Db 181 IDWDTSAAPYLGTQBECLFGLLTILFVLCVAATLLVAEEAALGPTPEAEGLSAPLSLSPH 240
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Db 241 CCPCRLAFRNIGALLPRLHQLCCMRPTLRLFVAELCSMMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLVA 360
Db 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLVA 360
QY 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMWSAAGLGLVAIYFATQ 540
Db 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMWSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 14
US-09-651-236-113
; Sequence 113, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651.236
; NUMBER OF SEQ ID NOS: 855
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-651-236-113
Query Match 100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLVCLAGITVVPPLLLLEVGVVEEKFTMTVLGIG 60
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Db 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLVA 360
QY 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGSGGLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMWSAAGLGLVAIYFATQ 540
Db 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMWSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553
RESULT 15
US-09-030-606-113
; Sequence 113, Application US/09030606
; Patent No. 6887660
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-606-113

Query Match      100.0%; Score 2861; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.5e-270;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MVQRLWVSRLLRHRKAQLLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60
Db      1 MVQRLWVSRLLRHRKAQLLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKEFTMWVLGIG 60

Qy      61 PVLGLVCVPLLGASDHWRGRRRPFYWALSGLILLSLFLIPRAGWLAGLLCPDPRL 120
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Qy      121 ELALLILGVGLDFCQGVCFPLEALLSDLFRDPDHCROQSVYAFMISLGGCLGYLLPA 180
Db      121 ELALLILGVGLDFCQGVCFPLEALLSDLFRDPDHCROQSVYAFMISLGGCLGYLLPA 180

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Db      241 CCPCRARLAFRNIGALLPRHLQCCRMPTLRRLFVAELCSWMLMTFTLFTYDFVGEGL 300

Qy      301 YQGVPRAEPTGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
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Qy      361 AFPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db      361 AFPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

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Qy      481 RVVPGRGICLDLAILDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
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Qy      541 VVFDKSDLAKYSA 553
Db      541 VVFDKSDLAKYSA 553
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Job time : 52 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2006, 04:05:48 ; Search time 183 Seconds
(without alignments)
1399.769 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHKAQLLL.....AIYFATQVVFDKSLAKYSA 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	553	US-09-745-288-101	Sequence 101, App
2	2861	100.0	553	US-09-838-785-2	Sequence 2, Appli
3	2861	100.0	553	US-09-759-143-113	Sequence 113, App
4	2861	100.0	553	US-09-780-669-113	Sequence 113, App
5	2861	100.0	553	US-09-030-606-113	Sequence 113, App
6	2861	100.0	553	US-09-822-827-113	Sequence 113, App
7	2861	100.0	553	US-09-115-453-113	Sequence 113, App
8	2861	100.0	553	US-09-232-880-113	Sequence 113, App
9	2861	100.0	553	US-09-895-793-113	Sequence 113, App
10	2861	100.0	553	US-09-895-814-113	Sequence 113, App
11	2861	100.0	553	US-10-012-896-113	Sequence 113, App
12	2861	100.0	553	US-10-010-940-113	Sequence 113, App
13	2861	100.0	553	US-10-144-678A-113	Sequence 113, App
14	2861	100.0	553	US-10-005-907-13	Sequence 113, App
15	2861	100.0	553	US-10-294-025-113	Sequence 113, App
16	2861	100.0	553	US-10-295-027-548	Sequence 548, App
17	2861	100.0	553	US-10-295-027-902	Sequence 902, App
18	2861	100.0	553	US-10-453-919-101	Sequence 101, App
19	2861	100.0	553	US-10-688-838-113	Sequence 113, App
20	2861	100.0	553	US-10-403-142-2	Sequence 2, Appli
21	2861	100.0	553	US-10-936-626-99	Sequence 99, Appl
22	2861	100.0	553	US-10-938-061-99	Sequence 99, Appl
23	2861	100.0	553	US-10-732-923-24012	Sequence 24012, A
24	2861	100.0	553	US-11-234-786-113	Sequence 113, App
25	2861	100.0	1079	US-09-822-827-947	Sequence 947, App
26	2861	100.0	1079	US-09-895-793-947	Sequence 947, App
27	2798	97.8	553	US-10-732-923-24008	Sequence 24008, A

ALIGNMENTS

RESULT 1

US-09-745-288-101
; Sequence 101, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-745-288-101

Query Match	Best Local Similarity	100.0%	Score 2861	DB 3	Length 553
Matches 553	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
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DB	1	MVQRLWVSRLLRHKAQLLLVNLTLFGLVCLAAAGTYVPPLLLEVGVEKFMVVLGIG	60		Sequence 23903, A
QY	61	PVGLVCVPLLSASDHWRGRRRPPFTWALSLGILLSLFLIPRAGWLAGLILCPDRPL	120		Sequence 24009, A
DB	61	PVGLVCVPLLSASDHWRGRRRPPFTWALSLGILLSLFLIPRAGWLAGLILCPDRPL	120		Sequence 23904, A
QY	121	ELALLILGVGLDFCQVCFTPLEALLSLDFDPDHCROAYSVYAFMISLGGCLGYLLPA	180		Sequence 5, Appli
DB	121	ELALLILGVGLDFCQVCFTPLEALLSLDFDPDHCROAYSVYAFMISLGGCLGYLLPA	180		Sequence 1029, Ap
QY	181	IDWTSALAPYLGTOBECFLGILLTLIFLCVAATLLVABEAAALGPTPEAGLSAPLSPH	240		Sequence 708, App
DB	181	IDWTSALAPYLGTOBECFLGILLTLIFLCVAATLLVABEAAALGPTPEAGLSAPLSPH	240		Sequence 708, App
QY	241	CCPCRARLAFNLGALLPRLHQLCCMPRTLRLFVAELCSMMALMTFTLFYDFVGEGL	300		Sequence 708, App
DB	241	CCPCRARLAFNLGALLPRLHQLCCMPRTLRLFVAELCSMMALMTFTLFYDFVGEGL	300		Sequence 708, App
QY	301	YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA	360		Sequence 708, App
DB	301	YQGVPAEPTGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA	360		Sequence 708, App
QY	361	APFVAAGATCLGSHSAVVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420		Sequence 708, App

Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Qy 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
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Qy 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Qy 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 3
US-09-759-143-113
; Sequence 113, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9,4e-240; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;

Qy 1 MVORLWVSRLLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVEEKFMTMWLGIG 60
Db 1 MVORLWVSRLLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVEEKFMTMWLGIG 60
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Qy 241 CCPCRARLAFRNIGALLPRHLQCCRMPTLRLRFLVAELCSNMALMTFTLFTYDFVGEGL 300
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Db 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Qy 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIFYATQ 540
Qy 541 VVFDKSDLAKYSA 553
Db 541 VVFDKSDLAKYSA 553

RESULT 2
US-09-838-785-2
; Sequence 2, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; APPLICANT: Van Heuit, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838,785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 2
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-838-785-2

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9,4e-240; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0;

Qy 1 MVORLWVSRLLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVEEKFMTMWLGIG 60
Db 1 MVORLWVSRLLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVEEKFMTMWLGIG 60
Qy 61 PVGLGVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Db 61 PVGLGVCVPLLGASDHWGRYGRRRPFIWALSIGLILSLFLIPRAGWLAGLLCPDPRPL 120
Qy 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILGVLLDFCGQVCFPLEALLSDLPDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Qy 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Db 181 IDWDTSAALPYLGTQECLFGLLTILFTCVAAATLLVAEEAALGPTPEAGLSAPSLSPH 240
Qy 241 CCPCRARLAFRNIGALLPRHLQCCRMPTLRLRFLVAELCSNMALMTFTLFTYDFVGEGL 300
Db 241 CCPCRARLAFRNIGALLPRHLQCCRMPTLRLRFLVAELCSNMALMTFTLFTYDFVGEGL 300
Qy 301 YQGVPRAEPTGTEARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRFGRTRAVLASVA 360
Db 301 YQGVPRAEPTGTEARRHYDEGVMSGLGLFLOCAISLVFSLVMDRLVQRFGRTRAVLASVA 360
Qy 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420

US-09-030-606-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
DB 181 IDWDTSAALPYLGTQECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYDFVGEGL 300
DB 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
QY 361 AFPVAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 AFPVAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQTAYMVSAAGLGLVAIFYATQ 540
DB 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQTAYMVSAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553
RESULT 6
US-09-822-827-113
; Sequence 113, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 392
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-113
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
```

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QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
QY 181 IDWDTSAALPYLGTQECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
DB 181 IDWDTSAALPYLGTQECLFGLTLIFLTCVAATLLVAEEAALGPTPEAEGLSAPLSPH 240
QY 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYDFVGEGL 300
DB 241 CCPCRARLARFNLGALLPRLHQLCCRMPTLRLFVAELCSMMALMTFTLFYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGRVMSGLFLQCAISLVFSLVMDRLVQREGTRAVYLASVA 360
QY 361 AFPVAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 AFPVAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQTAYMVSAAGLGLVAIFYATQ 540
DB 481 RVVPRGICLDLAILDSAFLLSQVAPSLFMGSIIVQLSQTAYMVSAAGLGLVAIFYATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553
RESULT 7
US-09-115-453-113
; Sequence 113, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-115-453-113
Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
DB 1 MVQRLWSRLRHRKAQLLVNLTFGLVCLAAAGITYVPPLLLEVGVEEKFMTWVLGIG 60
QY 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVLGLVCVPLLGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVGLDFCGQVCFPLEALLSDLFRDPDHCRCQAYSVAFMISLGGCLGYLLPA 180
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QY 181 IDWDTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
DB 181 IDWDTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLARFRNLGALLPRLHQLCCMRPRTLRLRFLVAELCSMMALMTFTLFYTFDFVGEGL 300
DB 241 CCPCRARLARFRNLGALLPRLHQLCCMRPRTLRLRFLVAELCSMMALMTFTLFYTFDFVGEGL 300
QY 301 YQGVPAEPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
DB 301 YQGVPAEPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
DB 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 8

US-09-232-880-113

; Sequence 113, Application US/09232880

; Publication No. US20020182596A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.428C6

; CURRENT APPLICATION NUMBER: US/09/232,880

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 113

; LENGTH: 553

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-232-880-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVBEKFTMWLGIG 60
DB 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVBEKFTMWLGIG 60
QY 61 PVGLVCVPLLGASDHWGRYGRRRPFTWALSGLILLSLFLIPRAGWLAGLCCPDRPL 120
DB 61 PVGLVCVPLLGASDHWGRYGRRRPFTWALSGLILLSLFLIPRAGWLAGLCCPDRPL 120
QY 121 ELALLILGVLLDFCGQVCTPTEALLSDLFRPDHCRQAYSVAFMISLGGCGLYLLPA 180
DB 121 ELALLILGVLLDFCGQVCTPTEALLSDLFRPDHCRQAYSVAFMISLGGCGLYLLPA 180
QY 181 IDWDTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
DB 181 IDWDTSALAPYLGTQBECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
QY 241 CCPCRARLARFRNLGALLPRLHQLCCMRPRTLRLRFLVAELCSMMALMTFTLFYTFDFVGEGL 300

DB 241 CCPCRARLARFRNLGALLPRLHQLCCMRPRTLRLRFLVAELCSMMALMTFTLFYTFDFVGEGL 300
QY 301 YQGVPAEPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
DB 301 YQGVPAEPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA 360
QY 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 361 APFVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
DB 481 RVVPGRGICLDLAIDLSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 9

US-09-895-793-113

; Sequence 113, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 113

; LENGTH: 553

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-895-793-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVBEKFTMWLGIG 60
DB 1 MVQRLWVSRLRHRKAQLLVNLTLFGLVCLAAAGITYVPPLLLEVGVBEKFTMWLGIG 60
QY 61 PVGLVCVPLLGASDHWGRYGRRRPFTWALSGLILLSLFLIPRAGWLAGLCCPDRPL 120

Db 61 PVGLVVCVPLLGSDHWRGRRRPFIFWALSGLLSLFLIPRAGWLAGLLCPDRPL 120
Qy 121 ELALLILVGLLDFCGQVCFPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILVGLLDFCGQVCFPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Qy 181 IDWTSALAPYLGTOECLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTOECLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Qy 241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMLMTFTLFYTDVFGGL 300
Db 241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMLMTFTLFYTDVFGGL 300
Qy 301 YQGVPRAPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
Db 301 YQGVPRAPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
Qy 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Qy 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
Qy 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIYFATQ 540
Qy 541 VVFDKSLAKYSA 553
Db 541 VVFDKSLAKYSA 553

RESULT 10

US-09-895-814-113
; Sequence 113, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-895-814-113

Query Match 100.0%; Score 2861; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 9, 4e-240; Mismatches 0; Indels 0; Gaps 0;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVQRLWVSRLLRHRKAQALLVNLTLFGLLEVCLAAAGITVYVPPLLLEVGVEKEKMTWVLGIG 60
Db 1 MVQRLWVSRLLRHRKAQALLVNLTLFGLLEVCLAAAGITVYVPPLLLEVGVEKEKMTWVLGIG 60
Qy 61 PVGLVVCVPLLGSDHWRGRRRPFIFWALSGLLSLFLIPRAGWLAGLLCPDRPL 120
Db 61 PVGLVVCVPLLGSDHWRGRRRPFIFWALSGLLSLFLIPRAGWLAGLLCPDRPL 120
Qy 121 ELALLILVGLLDFCGQVCFPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Db 121 ELALLILVGLLDFCGQVCFPLEALLSDLRDPDHCRCQAYSVYAFMISLGGCLGYLLPA 180
Qy 181 IDWTSALAPYLGTOECLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Db 181 IDWTSALAPYLGTOECLFGLLLTLIFLTCVAATLLVAEEAALGPTPEAGLSAPLSLSPH 240
Qy 241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMLMTFTLFYTDVFGGL 300
Db 241 CCPCRARLAFLNGLALLPRLHQLCCRMPTLRLRFLVAELCSWMLMTFTLFYTDVFGGL 300
Qy 301 YQGVPRAPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
Db 301 YQGVPRAPGTEARRHYDEGVRMGSGLFLQCAISLVFSLVMDRLVQRFCTRAVYLASVA 360
Qy 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Db 361 APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
Qy 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
Db 421 ASSEDSLMTSFLPGPKGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGTEA 480
Qy 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIYFATQ 540
Db 481 RVVPRGICLDLALDLSAFLLSQVAPSLFMGSIVOLQSQTAYMVSAAGLGLVAIYFATQ 540
Qy 541 VVFDKSLAKYSA 553
Db 541 VVFDKSLAKYSA 553

RESULT 11

US-10-012-896-113
; Sequence 113, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-113

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLEVGVEEKMVTMLGIG 60
DB 1 MVORLWVSRLLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLEVGVEEKMVTMLGIG 60
QY 61 PVGLVCVPLGSGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLGSGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLLDFCQVCFTPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVLLDFCQVCFTPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQECFLGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWTSALAPYLGTQECFLGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY 241 CPCRARLAFRNIGALLPRLHQLCCRMPTLRLFVAELCSNMALMTFTLFTYDFVGEGL 300
DB 241 CPCRARLAFRNIGALLPRLHQLCCRMPTLRLFVAELCSNMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
QY 361 APPVAAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG 420
DB 361 APPVAAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDIALDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVLIYFATQ 540
DB 481 RVVPGRGICLDIALDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVLIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 12

US-10-010-940-113
; Sequence 113, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-113

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVORLWVSRLLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLEVGVEEKMVTMLGIG 60
DB 1 MVORLWVSRLLRHRKAQLLVNLITFGLEVCLAAGITYVPPLLEVGVEEKMVTMLGIG 60
QY 61 PVGLVCVPLGSGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
DB 61 PVGLVCVPLGSGASDHWGRYGRRRPFIWALSIGILLSLFLIPRAGWLAGLLCPDPRPL 120
QY 121 ELALLILGVLLDFCQVCFTPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
DB 121 ELALLILGVLLDFCQVCFTPLEALLSDLPDPDHCROAYSVYAFMISLGGCLGYLLPA 180
QY 181 IDWTSALAPYLGTQECFLGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
DB 181 IDWTSALAPYLGTQECFLGLLTLFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
QY 241 CPCRARLAFRNIGALLPRLHQLCCRMPTLRLFVAELCSNMALMTFTLFTYDFVGEGL 300
DB 241 CPCRARLAFRNIGALLPRLHQLCCRMPTLRLFVAELCSNMALMTFTLFTYDFVGEGL 300
QY 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
DB 301 YQGVPRABPGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRFGTTRAVYLASVA 360
QY 361 APPVAAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG 420
DB 361 APPVAAGATCLSHSAVVTASAAALTGFTFSALQILPYTLASLVHREKQVFLPKYRGDTGG 420
QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
DB 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
QY 481 RVVPGRGICLDIALDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVLIYFATQ 540
DB 481 RVVPGRGICLDIALDSAPLLSQVAPSLFMGSIIVQLSQSVTAYMVSAAGLGLVLIYFATQ 540
QY 541 VVFDKSDLAKYSA 553
DB 541 VVFDKSDLAKYSA 553

RESULT 13

US-10-144-678A-113
; Sequence 113, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.

; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kaos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-113

Query Match 100.0%; Score 2861; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 9.4e-240;
Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVORLWVSRLRRKKAQLLVNLLTFCLEVCVLAAGITYVPPLLEVGVEEKFMTMVLGIG	60
Db	1	MVORLWVSRLRRKKAQLLVNLLTFCLEVCVLAAGITYVPPLLEVGVEEKFMTMVLGIG	60
Qy	61	PVLGLVCVPLLGSADHWGRGRRRPFITWALSIGILLSLFLIPRAGWLAGLLCPDPRPL	120
Db	61	PVLGLVCVPLLGSADHWGRGRRRPFITWALSIGILLSLFLIPRAGWLAGLLCPDPRPL	120
Qy	121	ELALLILGVLGLDFCGQVCFPTLEALLSDLFDRPDHCRQAYSYYAFMISLGGCLGYLLPA	180
Db	121	ELALLILGVLGLDFCGQVCFPTLEALLSDLFDRPDHCRQAYSYYAFMISLGGCLGYLLPA	180
Qy	181	IDWDTSAALPYLQTBECPLGGLTLFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH	240
Db	181	IDWDTSAALPYLQTBECPLGGLTLFLTCVAATLLVABEAAALGPTPEAGLSAPLSPH	240
Qy	241	CCPCRLARLAFRNIGALLPRHLQCCRMPTRLRLFVAELCSWMAWMTFTLFYTFDFVGEGL	300
Db	241	CCPCRLARLAFRNIGALLPRHLQCCRMPTRLRLFVAELCSWMAWMTFTLFYTFDFVGEGL	300
Qy	301	YQGVPRAEPTGEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA	360
Db	301	YQGVPRAEPTGEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFQTRAVYLASVA	360
Qy	361	APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Db	361	APPVAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG	420
Qy	421	ASSEDSIMTSFLPGPKGAPFPNGHVCGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA	480
Db	421	ASSEDSIMTSFLPGPKGAPFPNGHVCGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA	480
Qy	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ	540
Db	481	RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAAGLGLVAIYFATQ	540
Qy	541	VVFDKSDLAKYSA 553	
Db	541	VVFDKSDLAKYSA 553	

Search completed: May 27, 2006, 04:09:37
Job time : 185 secs

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OM protein - protein search, using sw model

Run on: May 27, 2006, 04:06:44 ; Search time 15 Seconds
(without alignments)
410.596 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

Sequence: 1 MVQLWVSLRRHRAQLL.....AIVFATQVVDKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	323.5	11.3	507	6	US-10-953-349-4710 Sequence 4710, Ap
2	323.5	11.3	512	6	US-10-953-349-4709 Sequence 4709, Ap
3	313	10.9	511	6	US-10-953-349-13600 Sequence 13600, A
4	312	10.9	475	6	US-10-953-349-13601 Sequence 13601, A
5	274.5	9.6	434	6	US-10-953-349-4711 Sequence 4711, Ap
6	177	6.2	351	6	US-10-953-349-13602 Sequence 13602, A
7	129	4.5	240	6	US-10-953-349-18828 Sequence 18828, A
8	126	4.4	228	6	US-10-953-349-18830 Sequence 18830, A
9	126	4.4	230	6	US-10-953-349-18829 Sequence 18829, A
10	113	3.9	1403	6	US-10-505-928-471 Sequence 471, App
11	103.5	3.6	537	6	US-10-953-349-31157 Sequence 31157, A
12	103.5	3.6	550	6	US-10-953-349-31156 Sequence 31156, A
13	103.5	3.6	584	6	US-10-953-349-31155 Sequence 31155, A
14	100	3.5	342	6	US-10-953-349-33245 Sequence 33245, A
15	99	3.5	443	6	US-10-953-349-37180 Sequence 37180, A
16	97.5	3.4	245	6	US-10-953-349-26339 Sequence 26339, A
17	95.5	3.3	1443	7	US-11-293-697-3844 Sequence 3844, Ap
18	93.5	3.3	442	6	US-10-953-349-2567 Sequence 2567, Ap
19	93.5	3.3	439	6	US-10-953-349-2566 Sequence 2566, Ap
20	92.5	3.2	391	6	US-10-953-349-37182 Sequence 37182, A
21	92.5	3.2	416	6	US-10-953-349-37181 Sequence 37181, A
22	92	3.2	403	6	US-10-953-349-5592 Sequence 5592, Ap
23	91	3.2	424	6	US-10-953-349-11588 Sequence 11588, A
24	91	3.2	460	6	US-10-953-349-11587 Sequence 11587, A
25	91	3.2	486	6	US-10-953-349-11586 Sequence 11586, A

ALIGNMENTS

RESULT 1

US-10-953-349-4710 440 7 US-11-302-678-41 Sequence 41, Appli
; Sequence 4710, Application US/10953349 Sequence 3, Appli
; Publication No. US20060107345A1 Sequence 14670, A
; GENERAL INFORMATION: Sequence 14, Appli
; APPLICANT: ALEXANDROV, Nickolai et al. Sequence 27707, A
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES Sequence 27706, A
; FILE REFERENCE: 2750-1579PUS2 Sequence 27705, A
; CURRENT APPLICATION NUMBER: US/10/953,349 Sequence 2568, Ap
; CURRENT FILING DATE: 2004-09-30 Sequence 36050, A
; NUMBER OF SEQ ID NOS: 40252 Sequence 36059, A
; SOFTWARE: PatentIn version 3.3 Sequence 3831, Ap
; SEQ ID NO 4710 Sequence 3830, Ap
; LENGTH: 507 Sequence 2, Appli
; TYPE: PRT Sequence 31943, A
; ORGANISM: Arabidopsis thaliana Sequence 31942, A
US-10-953-349-4710 Sequence 28815, A
Sequence 28814, A
Sequence 31944, A
Sequence 266, App
Sequence 771, App

Query Match	11.3%	Score 323.5;	DB 6;	Length 507;
Best Local Similarity	24.1%	Pred. No. 86-20;		
Matches 123;	Conservative 92;	Mismatches 195;	Indels 101;	Gaps 18;
QY	14	RKAQLLVNLLTFGLVCLAAAGITYVPPLLLEVGVEEKFMVWLGIQVPLGLVCVPLLGS 73		
Db	23	RURKIISVSSIAAGVQFGWALQLSLTPYVQLLGIPIHKWASLIWLCCGPISGMLVQPIVGY 82		
QY	74	ASDHWGRYGRRRPPTIWAISLILSLFLIPRAGWLAGL-----LCPDPRPLEALLI 126		
Db	83	HSDRCTSREGRRRPPIVAGAGIVTVAVFLI---GYAADIGHSGDGLDKPKPKTRAIIFA 139		
QY	127	LGVLGLDFCGQVCFPTPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL 178		
Db	140	LGFWILDVANNTLQGPCRAFLADLSAGNAKKTETANAFSFFMAVGNVLGYAAGSYENLY 199		
QY	179	PAIDWD-TSALAPYLGTOBECIFGLTLTLPFCVAATLLVABEALGPTPEBGLSAPSL 237		
Db	200	KVPFPTMTSCDLYCANLKTCFFLSITLL-LIVTFVSLCYVKEKPMPTPEPTADGKA---- 254		
QY	238	SHPCPCRLARLAFRLGALLPRHLQOLCCRPRTLRLFVAELCSWMLMTFTLFYDFVG 297		
Db	255	-----SNVPF--FGEIFGAFKEL-----KRPMMMLLIVTALNWTANFPFLFDFTDWMG 300		
QY	298	EGLYQGVPAEPGCTEARRHYDEGVRMGSLGLFQCAISLVFSLVMDRLVQRFCTRAVYLA 357		
Db	301	REVYGNSDATATASKLYNDGVAGALGLMLNAIVLGFMSLGVENIGRKLIG-GAKRLW 359		
QY	358	SVAAPFPAAGATCLSHSVAV-----VTASA-----ALTG-----FT 388		

ug-09-593-793a-113.rapbn

Tue May 30 15:28:26 2006

Db	360	GIVNFIL--AICLAMTVVTVKQAEHNRRDHGGAKTGGPGNVNTAGALTFLFAILGIPQAIT	416
Qy	389	FSALQILPYTLASLYHREK-----QVFLPKYRGDGTGGASSEDSLMTSFLPGP	435
Db	417	FS-----IPALASISTFSTNGAGQGLSLGVNLAIIVFQWISVGGGFDFELFGGGINPA-	471
Qy	436	KPCAPPNGNHVGAGSGLL-----PPPPA	459
Db	472	-----FVLGAIAAAVSGVLALTVLPSPPDA	497

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RESULT 2
US-10-953-349-4709
; Sequence 4709, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4709
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4709

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Query Match	11.3%;	Score 323.5;	DB 6;	Length 512;
Best Local Similarity	24.1%;	Pred. No. 8.1e-20;		
Matches 123;	Conservative 92;	Mismatches 195;	Indels 101;	Gaps 18;
QY	14	RKAQLLLVNLITFGLEVCLARAGITVVPFLLLEVGEKFTMVLIGVGLVLCVPLIGS	73	
DB	28	RLRKIISSVSSAAGVQFGMALQLSLTTPVQLLGIPHKWASLIWLCGVPSGMLVQPIVGY	87	
QY	74	ASDHWGRGYGRRRPTIWALSIGILLSLFLIPRAGWLAGL-----LCPDRPPELEALLI	126	
DB	88	HSDRCTSRFGRRRPFIVAGAGLVTVVAVFLI---GYAADIGHSGMDQLDKPKETRAIAIFA	144	
QY	127	LGVGILLDFCGQVCFPTPEALLISDLPR-DPDHCRQAYSVYAFMISLGGCLGY-----LL	178	
DB	145	LGFWILLVANNTLQGPCRAFADLSAGNAKKTRTANAFSFFMAVGNVLGYAAGSYRNLY	204	
QY	179	PAIDWD--TSALAPYLGTOECLFGLLTILITFCVVAATLLVABEAAALGTEPAEGLSARSL	237	
DB	205	KVPFTMTESCDLYCANLKTCFFLSITILL-LIIVFVSLCYVKEKPTWPTPTADGKA----	259	
QY	238	SPHCPCPCARLAFRNLGALLPRLHOLCCMPPTLRLFVAELCSWMAIMTFTFLFVDFVG	297	
DB	260	-----SNVPF--FGEIFGAFKEU-----KRPMMNLLIIVTALNWIANFPELLPDTDMWG	305	
QY	298	EGLYQGVPRAEPGTEBARRHYDEGVRMGSLGLFLOCAISLVFSLVMDRLVQRFGTSAVYLA	357	
DB	306	REVYCGNSDATATAASKKLYNDGVAGALGLMLNAIVLGFMSLGVIEWIGRKLK-GAKRLW	364	
QY	358	SVAAPFVAAGATCLSHSVAV-----VTASA-----ALTG-----FT	388	
DB	365	GIYNFETL---AICLAWTVVVTROAENHRDHGAKTGPNGNVTAGALTFLALGLTPOAIT	421	
QY	389	FSALQTLVPTLASLVHREK-----QVFLPKYRGDTGGGASDSLSMTSFLPGP	435	

RESULT 3

US-10-953-349-13600

; Sequence 13600, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 13600

; LENGTH: 511

; TYPE: PRT

; ORGANISM: Glycine max

US-10-953-349-13600

Query Match 10.9%; Score 313; DB 6; Length 511;

Best Local Similarity 24.2%; Pred.No. 6.1e-19;

Matches 141; Conservative 78; Mismatches 205; Indels 158; Gaps 23;

QY 17 QLLVNLFTGLEVCIAAGITYPPILLEVGVEEKPMTWLGLGCPVLGLVCVPLLGASD 76

DB 36 KMPAVASIAAGIQFGWALQSLTTPVQLLGVPHAAASFILWCGPISLWLVQPIVGYSD 95

QY 77 HWRGRYRRRPPFTWALSGLTLLSLFLIPRA---GWLAG-LLLCPDPRPLELALILGVGLL 132

DB 96 HCTSRGRRRPPFILGALAVAVAVFLIGYAADIGYAAGDDISKTTRPRVGVFVIGFWIL 155

QY 133 DFCQVCVFTPLEALLSDLFR-DPHCRQAVSVVAFMISLGGCLGY-----LLPAI 181

DB 156 DVANNMLQGPCRAFLADLAAGDQDKTRIANGFFSFMAVGNVLGYAAGSYKGLHMKPFT 215

QY 182 DWTDSALAPYLCTQEEC-LFGLLTFLFTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240

DB 216 --ETKACDVFCAMLKSCFFSILLLLFLAIVA--LLYVKQKV---EARALD-DATQPS 266

QY 241 CCPCRARLAFRNLGALLPRHLQLCRRMPRTLRLFVAELCSWMALMTFTLTPTDFVGEGL 300

DB 267 C-----FFQLFSALKEL-----KRPMMMLMLVTAVNMVGMFFYFLFDTDMMGREV 311

QY 301 YQGVPRAPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRL-----VQR----- 348

DB 312 YGG---QVGEDA---YANGVRVSGSLGMVNAVVLGPMNSLAVEPLGKMGVGVKRLWAINV 364

QY 349 -----FGTRAVYLASVAAPFVAAGATCLSH-SVAVVTASAAITG-----FTFSAIQI 394

DB 365 FILAIGF-MTVVITKVAEHQKKNPAAGVHPSEGVVGVSMVFFGVGLVPLAITFS----- 419

QY 395 LPYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKPGAPFNHGVHAGGSGLL 454

DB 420 VPFALASTY-----GAGQGLSLGLNLAINVPMVVTSLSGPWD 462

QY 455 PPPFALCGASACDYSVRVVVGEPTEARVVPGRGICLDLAILDSAPLLSQVAPSLFPMGSIV 514

DB 429 -----CSAS-----GAGQGLSLGLNLAINVPMVVTSLSGPWD 462

QY 515 QL---SQSVTAYMVSAAGLGLVAIYFATQVFDK-SDLAKYSA 553

DB 463 ALFGGNNLPAPMVWGAAALSAIMAILVLLPTPKPADEAKASS 504

RESULT 4

US-10-953-349-13601

; Sequence 13601, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349


```

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18828
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18828

Query Match      4.5%; Score 129; DB 6; Length 240;
Best Local Similarity 22.5%; Pred. No. 0.00058;
Matches 71; Conservative 33; Mismatches 94; Indels 118; Gaps 12;

QY 267 MPTLRRLRFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGL 326
DB 7 LKRPMMMLMTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGL 59

QY 327 GLFLOCAISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGA 368
DB 60 GLMNVAVVGLFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMN 118

QY 369 TGLSLH-SVAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 119 AAVGHPSEGVVGVSMVFFGLVGLPLAITFS---VPPALASIY----- 157

QY 421 ASSDSLMTSLFLPGPKGAPFNGHVAGGSGGLLPPPPALCGASACDVSVRVVVGEPT 480
DB 158 -----CSAS----- 161

QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 538
DB 162 ----GAGQGLSLGLVNLAIWVPQMVVSTLSGPDALFGGGLNLPAPFMVGAASAI 217

QY 539 TQVVFDPK-SDLAKYSA 553
DB 218 VLLPTPKPADEAKASS 233

RESULT 8
US-10-953-349-18830
; Sequence 18830, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18828
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18828

Query Match      4.5%; Score 129; DB 6; Length 240;
Best Local Similarity 22.5%; Pred. No. 0.00058;
Matches 71; Conservative 33; Mismatches 94; Indels 118; Gaps 12;

QY 267 MPTLRRLRFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGL 326
DB 7 LKRPMMMLMTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGL 59

QY 327 GLFLOCAISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGA 368
DB 60 GLMNVAVVGLFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMN 118

QY 369 TGLSLH-SVAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
DB 119 AAVGHPSEGVVGVSMVFFGLVGLPLAITFS---VPPALASIY----- 157

QY 421 ASSDSLMTSLFLPGPKGAPFNGHVAGGSGGLLPPPPALCGASACDVSVRVVVGEPT 480
DB 158 -----CSAS----- 161

QY 481 RVVPGRGICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 538
DB 162 ----GAGQGLSLGLVNLAIWVPQMVVSTLSGPDALFGGGLNLPAPFMVGAASAI 217

QY 539 TQVVFDPK-SDLAKYSA 553
DB 218 VLLPTPKPADEAKASS 233

RESULT 9
US-10-953-349-18829
; Sequence 18829, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18829
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18829

Query Match      4.4%; Score 126; DB 6; Length 230;
Best Local Similarity 22.7%; Pred. No. 0.00099;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 4 LMLVTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLGLMNV 56

QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGATCLSH-S 374
DB 55 VLGFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 113

QY 375 VAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSED 427
DB 114 EGVVGVSMVFFGLVGLPLAITFS---VPPALASIY----- 145

QY 428 MTSFLPGPKGAPFNGHVAGGSGGLLPPPPALCGASACDVSVRVVVGEPT 487
DB 146 -----CSAS-----GAG 152

QY 488 ICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 545
DB 153 QGLSLGLVNLAIWVPQMVVSTLSGPDALFGGGLNLPAPFMVGAASAIWAILLLPTPK 212

QY 546 -SDLAKYSA 553
DB 213 PADEAKASS 221

RESULT 9
US-10-953-349-18829
; Sequence 18829, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18829
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18829

Query Match      4.4%; Score 126; DB 6; Length 230;
Best Local Similarity 22.7%; Pred. No. 0.00099;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 4 LMLVTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLGLMNV 56

QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGATCLSH-S 374
DB 55 VLGFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 115
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; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18830
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18830

Query Match      4.4%; Score 126; DB 6; Length 228;
Best Local Similarity 22.7%; Pred. No. 0.00098;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 2 LMLVTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLGLMNV 54

QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGATCLSH-S 374
DB 55 VLGFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 113

QY 375 VAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSED 427
DB 114 EGVVGVSMVFFGLVGLPLAITFS---VPPALASIY----- 145

QY 428 MTSFLPGPKGAPFNGHVAGGSGGLLPPPPALCGASACDVSVRVVVGEPT 487
DB 146 -----CSAS-----GAG 152

QY 488 ICLDLAILDSAPLLSQVAPSLFMGSIVOL--SQSVTAYMVSAAGLGLV 545
DB 153 QGLSLGLVNLAIWVPQMVVSTLSGPDALFGGGLNLPAPFMVGAASAIWAILLLPTPK 212

QY 546 -SDLAKYSA 553
DB 213 PADEAKASS 221

RESULT 9
US-10-953-349-18829
; Sequence 18829, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18829
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18829

Query Match      4.4%; Score 126; DB 6; Length 230;
Best Local Similarity 22.7%; Pred. No. 0.00099;
Matches 70; Conservative 31; Mismatches 90; Indels 118; Gaps 12;

QY 274 LFVAELCSMMALMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVMSGLFLQCA 333
DB 4 LMLVTAVNVWGWFFYFLFTDMMGREVYGG---QVGEDA---YANGVRVGSGLGLMNV 56

QY 334 ISLVFSLVMDRL-----VQR-----FGTRAVVLASVAAPFVAAGATCLSH-S 374
DB 57 VLGFMSLAVEPLGKMGVGVKELWAINFILAIGFG-MTVVITKVAEHQKMNPAAVGHPS 115
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QY 375 VAVVTASALTG-----FTFSALQILPYTLASLYHREKQVFLPKYRGDTGGASSEDLSL 427
DB 116 EGVVGVSWVFGVLGVLPLAITFS-----VFFALASLY----- 147
QY 428 MTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSRVVVVGPEPTARVVPGRG 487
DB 148 -----CSAS-----GAG 154
QY 488 ICLDLAILDSAPLLSQVAPSLFMSIVQL--SQSTAYWVSAGLGLVAIFYATQVVDK 545
DB 155 QGLSGVLNLAIWVPMQVSTLSGPDALFGCGNLPAPFMVGAAGAAALSAIMAIVLLTPK 214
QY 546 -SDLAKYSA 553
DB 215 PADEAKASS 223
RESULT 10
US-10-505-928-471
; Sequence 471, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 471
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-471
Query Match 3.9%; Score 113; DB 6; Length 1403;
Best Local Similarity 21.4%; Pred. No. 0.1; Mismatches 175; Indels 152; Gaps 21;
Matches 104; Conservative 55;
QY 47 GVEEFMTMVLGIGPVGLGVCVPLLSASDHWGRYGRRRPFIWALSIGILLS--LFLIP 104
DB 828 GVHELLLIVITWGVISLVCLAICITFCFPRGLQSDRNTHKNLINLFIABIFLIG 887
QY 105 RAGWAGLLCPDRPLEALLILGVLLDFCGQVCF-----TPLEALLSDFRDPDHC 157
DB 888 IDTKYAIACP-----IFAGLLHFFFLAFAFWMLCGVQLYMLLVEVF-ESEYS 935
QY 158 ROAYSVYAFMISLGGCLGVLLPAIDWDTALAPY--LGTQEEC----- 198
DB 936 RKXYVYA-----GYLFATVVGVSAAIDYKSGTEKACWLHVDNYFTWSTFGPVT 986
QY 199 LFGLLTLFLTCVAATLVAEEAALGPTPEAEGLSAPLSHCCPCRARLAFRLNGLALIP 258
DB 987 FIILLNIIFLV-ITLCKWVKHNTLKPDS-----SRL--ENIKSWVL 1025
QY 259 RLHQLCRMPRT--LRLRFVAELCSMMALMTTFLTYDFVGGELY----- 301
DB 1026 GAFALLCLLGLTWSFGLLFINETIVMAYL-FTIF-NAFQGVFIIFHICALQKVRKEYG 1083
QY 302 -----QGVRAEP-----GTEA--RHDEYGVRMGSLGFLQCA 333
DB 1084 KCFRHSYCCGLPTSPSHSSVKASTRTSARVSSGTQSRIRRMWMDTVRKQSESSFISGD 1143
QY 334 ISLVFSL-----VMDRLVQRFGRTRAVLASVAAPFAAGATCLSHSVAVTA 380
DB 1144 INSTLNQGHSLNARDTSANDTLPLNGFNNSYSLHKGDY-----NDSVQVDC 1194
QY 381 SAALTGFTFSALQILPYTLASLYHREK-----QVFLPKYRGDTGGASSED-----SLM 428
DB 1195 GLSLNDTAFKMIISLVHNNLRGSKTHNLELTLF-VKPVITGGSSSEDDAIVADASSLM 1253

QY 429 TSFLPG 434
DB 1254 HSDNPG 1259
RESULT 11
US-10-953-349-31157
; Sequence 31157, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31157
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31157
Query Match 3.6%; Score 103.5; DB 6; Length 537;
Best Local Similarity 22.3%; Pred. No. 0.2;
Matches 128; Conservative 61; Mismatches 225; Indels 161; Gaps 29;
QY 33 AAGITYVPPLLLEVGVEEKFMVLG-TGPVLGLVCVPLLSASDHWGRYGRRRPFIWA 91
DB 26 AANFAPIPGALIADMYTGRFMAISLSIACLTGV-----FLW- 63
QY 92 LSLGILLSLFLIPRAG-WLAGLLCPDRPLEALLILGVLLDFCGOVCFPLE-ALLSD 149
DB 64 --LSAMIPGARPPPCGVGLAGEQCAPPGRHLAWLIAGTFPLSI-GAGGIRPCSMWAFGAD 120
QY 150 LP-RDPDCHR-----QAYSVYAFMISLG-----GCLGYLLPAIDWDTALAPYLGTQBE 197
DB 121 QFSRHPKERRSRILQAY-FNAYVASIGVAFTVAVTVVQDNVGMKAGFAVP----- 172
QY 198 CLFGLLLTLIFTCVAATLLVAEEAALGPTPEAEGLSAPLSHCCPCRARLAFRLNGLALL 257
DB 173 --MGLMMLSAVSFLIGLSRLYVKEK--GSKMPAGIGAALVA-----AIRNRYVOL 218
QY 258 PRL-----HQLCCRMPRTLRL--FVAELCSMMALMTTFLTYDFVGGELYQGVRAEP 309
DB 219 PAKTEGTVYHHLKCKLTVPTDRLRPLNKAC-----IISNNGVDL-----P 260
QY 310 GTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGRTRAVLASVAAPFAAGAT 369
DB 261 GTGAA-----ASERDGNVGRRLCTVDQVEQLKSAVRILPIMWSTVFLAQ----- 305
QY 370 CLSHSVAVVTA-----AALTGFTFSALQILPYTLASLYHREKQVFLPKY 414
DB 306 AMSQNYAVLQANEMDRRIGVGFVPGCSLTFFNFMVMSL-----MSGSYDRVIAPALRRV 361
QY 415 RGDTCGASSEDLSMTSFL-----PGPKCAPFPNGHVAGGSGL-----LPPPPALCG 462
DB 362 TGDPRGLTKORVGVGLLLATAMAVSGAVEGRRRRLLELAGGGGAGMSAFWLVPQFALMG 421
QY 463 ASACDVSVRVVVG-----PTEARVVPGRGICLDLAILDSAFLLSQVAPSLFM----- 510
DB 422 LA-----EAFVIGELEFFYTE---LPKSMASFMLLYAMGVGNLVNSLIVKVVDDASR 474
QY 511 --GSIVQLSQSVTA-----YMWVSAGLGLV-AIYF 537
DB 475 RGGRTSWLSSDLNAGHYDYVYVLLAGLGAIVNEVF 509
RESULT 12
US-10-953-349-31156
; Sequence 31156, Application US/10953349

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GenCore version 5.1.18
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2006, 03:59:53 ; Search time 42 Seconds
(without alignments)
1266.854 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHKAQLLL.....AIYFATQVVFDSKLAKYSA 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
1	347.5	12.1	sucrose-proton tra
2	337.5	11.8	sucrose transport
3	330	11.5	probable sucrose-p
4	328.5	11.5	sucrose transport
5	324.5	11.3	probable sucrose-p
6	323.5	11.3	sucrose transport
7	323.5	11.3	sucrose transport
8	317.5	11.1	sucrose transport
9	311	10.9	sucrose transport
10	305.5	10.7	sucrose-proton tra
11	297.5	10.4	sucrose transport
12	294	10.3	sucrose transport
13	294	10.3	sucrose-proton sym
14	292.5	10.2	probable sucrose t
15	282	10.2	probable sucrose t
16	286	10.0	hypothetical prote
17	281.5	9.8	probable sucrose-p
18	279.5	9.8	sucrose transport
19	276.5	9.7	probable sucrose-p
20	273	9.5	sucrose transport
21	235.5	8.2	probable sucrose c
22	191	6.7	hypothetical prote
23	187.5	6.6	transporter, proba
24	142	5.0	melibiose carrier
25	139.5	4.9	hypothetical prote
26	138.5	4.8	transporter P8217
27	136	4.8	membrane protein,
28	133	4.6	probable MFS trans
29	128.5	4.5	probable MFS trans

ALIGNMENTS			
RESULT 1			
T14340			
sucrose-proton transport protein - carrot			
N;Alternate names: sucrose/H+ symporter protein			
C:Species: Daucus carota (carrot)			
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
C:Accession: T14340			
R;Shakya, R.; Sturm, A.			
Plant Physiol. 118, 1473-1480, 1998			
A>Title: Characterization of source- and sink-specific sucrose/H+ symporters from carrot			
A:Reference number: Z17991; MUID:99063785; PMID:9847123			
A:Accession: T14340			
A>Status: preliminary; translated from GB/EMBL/DBBJ			
A:Molecule type: mRNA			
A:Residues: 1-515 <SHA>			
A:Cross-references: UNIPROT:O65803; UNIPARC:UPI0000009CB3F; EMBL:Y16768; NID:g2969883; P			
A:Experimental source: cultivar Namtaise; root			
C:Genetics:			
A>Note: SUT2			
C:Superfamily: common tobacco sucrose transport protein			
Query Match 12.1%; Score 347.5; DB 2; Length 515;			
Best Local Similarity 25.9%; Pred. No. 1.7e-18;			
Matches 131; Conservative 80; Mismatches 215; Indels 79; Gaps 17;			
QY	17	QLLLVNLTFGLGVCLAAGITVPPLLLEVGVEEKEFTMVLGIGVGLVCVPLLGASD	76
DB	34	KLVVAATAAGVQFGWALQSLTTPVQLGIPHKWAAVYIWLCPISGMLVQPIVGYSD	93
QY	77	HWGRYGRRRPTIWLISGLISLFLIPRAGLAGL-----LCDDPRPLELALLILGV	129
DB	94	HQCSFGRRRPTIASGAGCVASVILI---GFAADISYKAGDDMSKTLKPRATVTVVIGF	150
QY	130	GLLDFCGQVCTFPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL	178
DB	151	WILDVANMLQGPCRALLADLCSGDTRRMRSAFYSPFMAVGNILGYAAGSYNNLYKLF	210
QY	179	PAIDWDTSALAPYLGTQECLEGLTLTLCVAATLLVAEEANLGPTEPAEGLSAPLS	238
DB	211	PFS--KTHACDLYCANLSCFIISIALLIITVVALSVVRENS--GPPDADAEEP----	263
QY	239	PHCCPCRLAPRNIGALLPRHLQCCRRPTRLRLRFVAELCSWMALMTFTLYTDFVGE	298
DB	264	----PSSGKIPV--FGELLGALKDL----PRMILLIIVTCLNWIWFFILFDTDMGR	313
QY	299	GLYQGVPRAPGTEARRHYDEGRVMSGLFLFOCALISLVFSLVMDRLVORFGTRAVLAS	358
DB	314	EIYGGT--AGQG---KLYDQGVRAALGGLLNSVVLGTLSTAVEYLVRGVGVKI-LWG	366
QY	359	VAAFPVAAGATCL-----SHSV-----AVTASA-----ALTGTFPSALQIL	395
DB	367	FVNFIATIGLVMTVVSVKVAQHQRHSANGQLLPPPSAGVKGALSLFSLIGIPLSITYSI	426

probable permease
resistance protein
probable integral
tetracycline resis
drug efflux protei
sugar transporter,
tetracycline prote
hypothetical prote
tetracycline-efflu
tetra protein - Pse
MFS permease (drug
probable efflux pr
hypothetical metab
multidrug-efflux t
puromycin resistan
hypothetical prote

Tue May 30 15:28:26 2006

396 PYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKPG-----APPNGHVGVA 448
 427 PFALASLYSSGSGAGQGLSLGVNLAIWVPMIVSVLWAGFFDSLFGGGLPAFVVGVAISA 486
 449 GSGGLP-----PPPALCGASACDVS 469
 487 AISGVLAIVLLPKPSKDAASKLSLS 511

RESULT 2
 T12198
 sucrose transport protein - fava bean
 C:Species: Vicia faba (fava bean)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T12198
 R:Weber,H.; Borisjuk, L.; Heim, U.; Sauer, N.; Wobus, U.
 Plant Cell 9, 895-908, 1997
 A:Title: A role for sugar transporters during seed development: molecular characterization
 A:Reference number: 217451; MUID:97355984; PMID:9212465
 A:Accession: T12198
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-523 <WEB>
 A:Cross-references: UNIPROT:O04077; UNIPARC:UPI00000A440D; EMBL:Z93774
 C:Genetics:
 A:Gene: sut
 C:Superfamily: common tobacco sucrose transport protein

Query Match 11.8%; Score 337.5; DB 2; Length 523;
 Best Local Similarity 25.8%; Pred. No. 9.5e-18;
 Matches 134; Conservative 76; Mismatches 185; Indels 125; Gaps 20;

QY 17 QLLVNLVTFGLEVCLAGITVPPVLLLEVGVEEKFTMTVLGIPGLVLCVPLGSASD 76
 DB 36 KIMVVASIAGVQGMALQLSLTTPYVQLLGHHTTAAIYIWLCPISGMVQPIGVHSD 95
 QY 77 HWRGRYGRRRPIWALSGLISLFLIPRAGWLAGL-----LCPDPRPLELALLIGV 129
 DB 96 RCTSFGRRRPIAAGSIAVAIAVELI--GVAADLGHSGDSDQKVRPRAIGIFVVG 152
 QY 130 GLLDFCGQVCTPPLBALLSDLER-DPDHCRQAYSVAFWISLGGCLGYLLPAID----- 182
 DB 153 WILDVANNMLOGPCRALLGDLCAGNQRTRNANAFSFFMAVGNVGLVGAAGAYSKLVHVF 212
 QY 183 --WDSALAPYLGTOBECFLGLTLTIFLTCVAATLLV-AEEAALGTEPA-----EGLSAP 235
 DB 213 PFTTKACNVYCANLKSCEF--LSIALTLVATSALIVYKETAFTPEVTVTEDGSSG 270
 QY 236 SLSPHCCPCRAL--APRNMGALLPRHLQCCMRPTLRRLFVLAELCSWMALMTFTLYT 293
 DB 271 GM-----PCFGSLSGAFKEL-----KRPMMILLVTLCLNIAFWPFLLED 311
 QY 294 DFVGEGLYQGVPRBEGTEARRH-YDEGVRMGSLGLFLQCAISLVSFLVMDRLVQFGR 352
 DB 312 DMWGKEVY-----GGTVGEGHAYDMGVREGALGLMLNSVVLGATSLGVDILARGVG-G 363
 QY 353 AVYLASVAAPVAAGATCLSHSVV-----TASALTGF 387
 DB 364 VKRLMGIVNELL--AICLGLTVLTKLAHQSHROYAPGTGALGDLPLPPSEGIKALUTIF 420
 QY 388 TFSALQI-----LPYTLASLYHREKQVFLPKYRGDTGGASSEDLS-----MTS 430
 DB 421 SVLGVPALATYISPPALASIF-----SSTSGAGQGLSLGVNLAIWVPMFVS 468
 QY 431 FLPGPKPG-----APPNGHVGAGSG-----LLPPPP 458
 DB 469 VLSGPPDALFGGGLNPAFVVGVAALASGILSILLPSP 508

C:Species: Solanum tuberosum (potato)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JQ2389; S40310
C:Riesmeier, J.W.; Hirner, B.; Frommer, W.B.
Plant Cell 5, 1591-1598, 1993
A:Title: Potato sucrose transporter expression in minor veins indicates a role in phloem loading
A:Reference number: JQ2389; MUID:94146554; PMID:8312741
A:Accession: JQ2389
A:Molecule type: mRNA
A:Residues: 1-516 <R1E>
A:Cross-references: UNIPROT:Q43633; UNIPARC:UPI000009FF9P; EMBL:X69165; NID:9439293; P11
A:Experimental source: cv. Desiree
C:Comment: The gene encoding for this protein is highly expressed in mature leaves.
C:Superfamily: common tobacco sucrose transport protein
C:Keywords: glycoprotein; transmembrane protein
F:31-53/Domain: transmembrane #status predicted <TM1>
F:67-86/Domain: transmembrane #status predicted <TM2>
F:103-122/Domain: transmembrane #status predicted <TM3>
F:141-160/Domain: transmembrane #status predicted <TM4>
F:180-200/Domain: transmembrane #status predicted <TM5>
F:226-248/Domain: transmembrane #status predicted <TM6>
F:285-304/Domain: transmembrane #status predicted <TM7>
F:331-349/Domain: transmembrane #status predicted <TM8>
F:366-385/Domain: transmembrane #status predicted <TM9>
F:409-427/Domain: transmembrane #status predicted <TM10>
F:429-448/Domain: transmembrane #status predicted <TM11>
F:3.92/Binding site: carbohydrate (Asn) #status predicted

	Query Match	11.5%	Score 330;	DB 2;	Length 516;															
	Best Local Similarity	24.7%;	Pred. No. 3.4e-17;																	
	Matches 132;	Conservative	Mismatches 197;	Indels 112;	Gaps 21;															
QY	4	RLWVSRLLRKQAQLLVNLT	TEGLVCLTAAGTYVP	PLLEVGVEEKFMT	VLGIGPVL 63															
DB	29	KLW	-----KIIIVASIA	QVQGNALQISL	TPYVQLLGIPHKFASFWL	CGPIS 78														
QY	64	GLVCPVLG	SADHWGRYGR	RRPFIIWALS	IGILLSLFLIP	RAGWLAGL	-----LCPD 116													
DB	79	GMI	VQPVGVY	YDNCSSRF	RRRRPFIA	AAGAALVIAVFLI	---GFAADLGHASG	DTLGKG 135												
QY	117	PRPLEALL	ILGVLLDF	CGOVCFTE	PLEALLSDL	FRDPD-HC	ROAVSVYAF	MI	SLGCLG 175											
DB	136	FKPRAIV	VVGVFWIL	VDANNL	OGPCRAL	LADLSGGK	SGEMRTAN	AF	FSFMAVGNILG 195											
QY	176	YLLPAIDW	-----DTSAL	AYLGTQE	ECFL-GL	LTLIFLT	CVATLL	VAE	-AALGP 225											
DB	196	YAAGSY	SHLFKVP	FFSKTK	CDMYCANL	KSCFFIAI	FLLSLTT	IALTL	VRENELPEKDE 255											
QY	226	TEPAEGL	SAPLS	PHCCPC	RARLAF	RNLGALL	PLRHOL	CCMRPT	RLRFLVAELCS	WMAL 285										
DB	256	QEIDEK	LAGAG	-----KSKV	PF--FGEI	FGALKEL	-----PRP	MI	LLVTC	LNIAW 301										
QY	286	MTFTL	FYTD	FGEGLY	QVQV	PAEFGTE	ARRHYDE	GVRM	SLGLFL	QCASISL	VFLSVM	DRLL 345								
DB	302	FPFFLY	DTDM	WAKE	VEFG	-----QVGD	-ARLYD	LGVR	AGMGL	LLQSV	LVG	FMSL	GVLEFL 355							
QY	346	VORF	GTTR	AVYLA	SVNA	FPVA	AGATC	LSH	SVAVV	-----TASA	ALTGT	----- 388								
DB	356	GKKIG	-GAKRL	WGIL	NFLV	---AICL	AMTIL	VLTK	WAKS	ROHDP	AGTL	MGPT	PGVK	IGAL 411						
QY	389	--FSALQI	-----LPY	TLASL	YHREX	-----OV	FLPK	YR	GT	DTG	GG	ASSE	DS 426							
DB	412	LLFA	LGI	PLA	ATFSI	FPAL	ASIF	SSNR	GGSL	GVNL	IAIV	VVFW	MLSV	LG	WFP	DDLL 471				
QY	427	LMTS	FL	DPK	PG	KAP	FP	N	GHV	GGSG	-----LL	PP	PP	AL	CG	AS	CDV	SV	VR	VVVG 475
DB	472	FGG	N	LP	G	-----FV	GA	AAAA	AA	VA	AL	TW	LS	FP	PA	-----DA	K	PA	VA	WG 512

RESULT 4
G84441
probable sucrose-proton symporter [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Cross-references: UNIPROT:Q03411; UNIPARC:UPI0000136132; EMBL:X67125; NID:g21318; PID:
C;Superfamily: common tobacco sucrose transport protein
C;Keywords: transmembrane protein

	Query Match	11.3%;	Score 324.5;	DB 2;	Length 525;
	Best Local Similarity	23.2%;	Pred. No. 9.1e-17;	Mismatches 196;	Indels 141; Gaps 20;
	Matches 129;	Conservative			
Qy	23	LITFGLVCLAAAGITY-----VPPLLEEVGVEEKMTMVLGIGPVLGVLCVPLLGA 74			
Dd	35	LKKLGIVASVAAGVQFGWALQLSLTPYVQLLGIPTHTWAAYIWLCPGISGMIVQPLVGYY 94			
Qy	75	SDHWGRVGRRRPFTHALSIGILLSLFLPRAGWLA--GLLCPDP-----RPLEIALLL 127			
Dd	95	SDRCTSRGRRRPFFIAAGAALVAAGCLI---GFAADIGAASGDPTGNVAKPRATAVFVV 151			
Qy	128	GVGLDFDGOVCFTPLEALLSDLFR-DPDHCRQAYSVYAWISLGCGCLGYLLPAID---- 182			
Dd	152	GFWIILDVANNITQGPCRALLDMAAGSQTKTRYANAFPSFMALGNITGGYAAGSYRLYT 211			
Qy	183	---WDTSALAPYLGTQEBCFLGLLT-LIPTCVAAATLLVAEEAALGTEPAEGLSAPS 237			
Dd	212	VFPFTKTAACDYCANLKSCFFISITLLIVLTILALSVVKERQITIDEIQSEEDLNKNRN 271			
Qy	238	SPHCPCCARLARFNALGALLPRHLQCRCMPRTLRRLFVAELCSMMALMTTTLFTYDFVG 297			
Dd	272	SSGC---ARLPF--FGQLIGALKDL---PKPMLILLVTALNWIAMFWPELLFTDWMG 321			
Qy	298	EGLYGVRAPECTEARHYDEGRVMSGLFLQCAISLVSLVMDRLVQRFG--TRAVY 355			
Dd	322	KEVYGGT-----VGEGLKYDGWHAGLGLMTNSVVLGYSLSIEGLARMVGGAKRLWG 375			
Qy	356	LASVAAPFAAGATCLSHSAVVVTTASAALTGTFFSALOILPYTLASLYHREKQVLPKYR 415			
Dd	376	IWNIL-----AVCLAMTV-LVTKSAE-----HFRDSHHIM---- 405			
Qy	416	GDTGGASSEDLSMTSFLPGPKPPNGPHVHGAGGGLLPPPPALCGASACDVSVRVVVG 475			
Dd	406	-----GSADVPPPAPA--GVKGALAIFAIVLG 429			
Qy	476	EPTEARV-VP-----GRGICLDLAILDSAFLLSQV-----AP 506			
Dd	430	IPLAITFPIPFALASIFSASSGGQGLSLGLNLAIIVPQMVFVSVTGPMDMFGGNLP 489			
Qy	507	SLFMGSIVOLQSQTAY 523			
Dd	490	AFVUGVAATAVASVLSP 506			
RESULT 6					
G86360					
Probable sucrose-proton symporter SUC2 protein T22J18.12 - Arabidopsis thaliana					
C;Species: Arabidopsis thaliana (mouse-ear cress)					
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004					
C;Accession: G86360					
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso					
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressay, T.H.; Dewar, K.					
ansen, N.F.; Hughes, B.; Huizar, L.					
Nature 408, 816-820, 2000					
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.					
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziali,					
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.					
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,					
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.					
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.					
A:Reference number: A86141; PMID:21016719; PMID:11130712					
A:Accession: G86360					
A>Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-512 <STO>					
A:Cross-references: UNIPROT:080550; UNIPARC:UPI00000482AD; GB:AEO05172; NID:g3287687; P:					
C:Genetics:					
A:Map position: 1					

C;Superfamily: common tobacco sucrose transport protein
C;Keywords: sugar transport

Query Match 11.3%; Score 323.5; DB 2; Length 512;
Best Local Similarity 24.1%; Pred. No. 1e-16;
Matches 123; Conservative 92; Mismatches 195; Indels 101; Gaps 18;

QY 14 RKAQLLVNLLTFGLVCLAAAGITVYVPLLEVGVEEKFTMTVLGIGVGLVCVPLGLS 73
DB 28 RLKRIISVSSIAAGVQFGWALQSLLTPVQLLGIPIHKWASLIWLCGPISGMLVQPIVGY 87
QY 74 ASDHWRGRRRRPFIWALSGLILLSLELI PRAGWLAGL-----LCPDPRPLELALLI 126
DB 88 HSDRCTSRFRRRPFIWAGAGLVTVAVFLI---GYAADIGHSMGDQDKPKPKTRAIAPA 144
QY 127 LGVGLLDFCGQVCFPLEALLSDLFR-DPDHCRQAYSVAFMISLGGCLGY-----LL 178
DB 145 LGFWILDVANNTLQGPCRAFLADLSAGNAKKTRTANAFSPFMAVGNVLGYAAGSYRNLY 204
QY 179 PAIDWD-TSALAPYLGTOEECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPSL 237
DB 205 KVPFTMTESCDLYCANLKTCCFLSITLL-LIVTFVSLCYVKEKPTPEPTADGKA---- 259
QY 238 SPHCPCRARLAFRLNGLALLPRHLQCCRMPTLRRLFVAELCSNMALMTFTLFTDFVG 297
DB 260 -----SNVPP--FGEIFGAFKEL-----KRPMMMLLIIVTALNWIAPFPLETDMWG 305
QY 298 EGLYQGVPAEPGTEARRHYDEGVRMSGLGLFLOCAISLVFLVMDRLVORFGTRAVYLA 357
DB 306 REVYGGNSDATATAASKLYNDGVRAGALGLMNAIVLGFMSLGVWIGRKLKLG-GAKRLW 364
QY 358 SVAAPFVAAGATCLSHSVAV-----VTASA---ALTG---FT 388
DB 365 GIVNFIL---AICLAMTVVTVTKQAENHRDHGAKTGPNGNVTAGALTTLFAILGIPQAIT 421
QY 389 FSALQILPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTSFLPQP 435
DB 422 FS-----IPFALASIFSTNSGAGGSLGLVNLAIIVPQMVISVGGGPFDELFGGGINIPA- 476
QY 436 KEGAPFPNGHVAGGSGLL-----PPPPA 459
DB 477 -----FVLGAIAAAVSGVLALTVLPSPPDDA 502

RESULT 7
S38196
sucrose transport protein SUC2 - Arabidopsis thaliana
N;Alternate names: sucrose-proton symporter SUC2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38196; T00773
R;Sauer, N.K.
submitted to the EMBL Data Library, October 1993
A;Description: SUC1 and SUC2: two sucrose transporters from Arabidopsis thaliana.
A;Reference number: S38196
A;Accession: S38196
A;Molecule type: mRNA
A;Residues: 1-512 <SAU>
A;Cross-references: UNIPROT:Q39231; UNIPARC:UPI00000A9ABE; EMBL:X75382; NID:g407091; PID:R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence.
A;Reference number: Z14202
A;Accession: T00773
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-490, 'A', 492-512 <VYS>
A;Cross-references: UNIPARC:UPI00000482AD; EMBL:AC003979; NID:g3172156; PID:g3287687; GS
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: SUC2; ATSP:T22J18.12
A;Map position: 1
A;Introns: 419/3; 441/1; 455/3

C;Superfamily: common tobacco sucrose transport protein
C;Keywords: sugar transport

Query Match 11.3%; Score 323.5; DB 2; Length 512;
Best Local Similarity 24.1%; Pred. No. 1e-16;
Matches 123; Conservative 92; Mismatches 195; Indels 101; Gaps 18;

QY 14 RKAQLLVNLLTFGLVCLAAAGITVYVPLLEVGVEEKFTMTVLGIGVGLVCVPLGLS 73
DB 28 RLKRIISVSSIAAGVQFGWALQSLLTPVQLLGIPIHKWASLIWLCGPISGMLVQPIVGY 87
QY 74 ASDHWRGRRRRPFIWALSGLILLSLELI PRAGWLAGL-----LCPDPRPLELALLI 126
DB 88 HSDRCTSRFRRRPFIWAGAGLVTVAVFLI---GYAADIGHSMGDQDKPKPKTRAIAPA 144
QY 127 LGVGLLDFCGQVCFPLEALLSDLFR-DPDHCRQAYSVAFMISLGGCLGY-----LL 178
DB 145 LGFWILDVANNTLQGPCRAFLADLSAGNAKKTRTANAFSPFMAVGNVLGYAAGSYRNLY 204
QY 179 PAIDWD-TSALAPYLGTOEECLFGLLTFLTCVAATLLVAEEAALGPTPEAGLSAPSL 237
DB 205 KVPFTMTESCDLYCANLKTCCFLSITLL-LIVTFVSLCYVKEKPTPEPTADGKA---- 259
QY 238 SPHCPCRARLAFRLNGLALLPRHLQCCRMPTLRRLFVAELCSNMALMTFTLFTDFVG 297
DB 260 -----SNVPP--FGEIFGAFKEL-----KRPMMMLLIIVTALNWIAPFPLETDMWG 305
QY 298 EGLYQGVPAEPGTEARRHYDEGVRMSGLGLFLOCAISLVFLVMDRLVORFGTRAVYLA 357
DB 306 REVYGGNSDATATAASKLYNDGVRAGALGLMNAIVLGFMSLGVWIGRKLKLG-GAKRLW 364
QY 358 SVAAPFVAAGATCLSHSVAV-----VTASA---ALTG---FT 388
DB 365 GIVNFIL---AICLAMTVVTVTKQAENHRDHGAKTGPNGNVTAGALTTLFAILGIPQAIT 421
QY 389 FSALQILPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTSFLPQP 435
DB 422 FS-----IPFALASIFSTNSGAGGSLGLVNLAIIVPQMVISVGGGPFDELFGGGINIPA- 476
QY 436 KEGAPFPNGHVAGGSGLL-----PPPPA 459
DB 477 -----FVLGAIAAAVSGVLALTVLPSPPDDA 502

RESULT 8
S48789
sucrose transport protein - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S48789
R;Buerkle, X.Y.Z.; Frommer, W.B.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48787
A;Accession: S48789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-507 <BUE>
A;Cross-references: UNIPROT:Q40583; UNIPARC:UPI00000A75A6; EMBL:X82276; NID:g575350; PID: submitted to the EMBL Data Library, October 1994
C;Superfamily: common tobacco sucrose transport protein

Query Match 11.1%; Score 317.5; DB 2; Length 507;
Best Local Similarity 24.3%; Pred. No. 2.9e-16;
Matches 125; Conservative 87; Mismatches 203; Indels 99; Gaps 18;

QY 4 RLWVSRLLRHRKAQQLLVNLLTFGLVCLAAAGITVYVPLLEVGVEEKFTMTVLGIGVPL 63
DB 23 KLW-----KIMVASIAAGVQFGWALQSLLTPVQLLGIPIHKFASFWLCCGIS 72
QY 64 GLVCPVPLLSGDHWRGRRRRPFIWALSGLILLSLELI PRAGWLAGLCCDDP-----R 118
DB 73 GMIVQPVVGYSDNCSSRRFRGRRGFIAGALVTVIAVFLIGFAADL-GHATGDLPGKGSK 131
QY 119 PLEALLIILGVGLLDFCGQVCFPLEALLSDLFRDPDHCRQAYSVAFMISLGGCLGYLL 178

Db 132 PRAIAVVFVGFWDVANNMLQGPCRALLADLSGGKARMTSNAFFSFFMAVGNVLGYAA 191
QY 179 PAID-----WDTALAPYLGTQBECLF-GLLTLIFLCVAATLLVAEEAALGTEPA 229
Db 192 GSYSRUCKIPFPSKTPACDIYCANLKSCEFIAVFLLLSUTILALT--VVRENELPEKDEH 249
QY 230 EGLSAPSLSPHCCPCRARLAFRNLGALLPRLHOLCCRMPTLRLRLFAELCSMMALMTFT 289
Db 250 E-----IDEKAGARSKVPF--FGEIFGALKDL-----PRPMWILLVTSLSNWIARFPFF 297
QY 290 LFYTDVFGSLGYGVPRAPSGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRP 349
Db 298 LYDITDWMKEVYGG--KVGDG-----RLYDLGVHAGALGLLNSVVLGFMFSLSVFELGKKI 351
QY 350 GTRAVVYLASVAAPFVAAAGATCLSHSVAVV-----TASAAITGFTFSALQI-- 394
Db 352 G-GVKRLWGLNLFV---AVCMALTVLVTQMAEKSQRYDAHGTLMAPTSGVKIGALTFLFA 407
QY 395 -----LPYTLASLYHREK-----QVFLPKYRGDTGGASSEDLSMTS 430
Db 408 VLGIPLAVTFSPFALASIFSSNAGSGQSLGLVNLAIWVPMQLVSIAGGPWDDLFGGG 467
QY 431 FLPGPKPGAPFNGHVGAGSG-----LIPPPPA 459
Db 468 NLPG-----FIVGAVAAASGILALTMLPSPPA 495

RESULT 9

S43142

sucrose transport protein - castor bean

N:Alternate names: sucrose carrier

C:Species: Ricinus communis (castor bean)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S43142

R:Weig, A.; Komor, E.

A:Description: A sucrose carrier from Ricinus communis.

A:Reference number: S43142

A:Accession: S43142

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-533 <WEI>

A:Cross-references: UNIPROT:Q41152; UNIPARC:UPI000009D016; EMBL:Z31561; NID:g468561; PID:113
C:Superfamily: common tobacco sucrose transport protein

Query Match 10.9%; Score 311; DB 2; Length 533;

Best Local Similarity 23.3%; Pred. No. 9.5e-16;

Matches 134; Conservative 95; Mismatches 225; Indels 120; Gaps 19;

QY 17 QLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVBEKFMVTLGIGPVGLVCVPLLSASD 76
Db 37 KVMVASIAGIQFGWALQSLTTPYVQLGIPHTWAAFIWLCGPISGMLVQVIVGHS 96
QY 77 HWRGRRRPPFTWALSGLILLSLFLIPRA---GWLAG-LLCPDPRPLELAILGVGLL 132
Db 97 RCTSRGRRRPPFTASGAFAVIAVFLIGYAADLHLSGDSLDKSPKTRAIAIPVGVF 156
QY 133 DFCGQVCTFPLEALLSDLF-RDPDHCROAVSVYAFMISLGGCIGYLLPAID-----W 183
Db 157 DVANNMLQGPCRALLADLSGTSQKTRTANALSFVFMVGNVLGYAAGAYTHLYKLPFT 216
QY 184 DTSALAPYLGTQBECLFGLTLIFLCVAATLLVAEEAALGTEPAEGL-----SAP 235
Db 217 KTTACDVYCANLKSCEFISIVLLSLTVALSVYKKEK-----PWSPPQADNAEDDTASQA 272
QY 236 SLSPHCCPCRARL--AFRNLGALLPRLHOLCCRMPTLRLRLFAELCSMMALMTFTFLFY 293
Db 273 SSSAQPMPPFGEILGAFKNL-----KRPMMILLVTLCLNMIANFPFLFDT 318
QY 294 DFVGEGLYGVPRAPSGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRF 353
Db 319 DWMGREVYGG--DSSGSAEQLKLYDRGVRAGALGLMLNSVVLGFTSLGVEVLARGVG-GV 375

RESULT 10

T14339

sucrose-proton transport protein - carrot

N:Alternate names: sucrose/H⁺ symporter protein

C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T14339

R:Shakya, R.; Sturm, A.

A:Title: Characterization of source- and sink-specific sucrose/H⁺ symporters from carrot

A:Reference number: Z17991; MUID:99063785; PMID:9847123

A:Accession: T14339

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-501 <SHA>

A:Cross-references: UNIPROT:O65929; UNIPARC:UPI000000ACFB6; EMBL:Y16766; NID:g2969886; P:1

A:Experimental source: cultivar Namtaise: leaf

C:Genetics:

C:Gene: SUT1a

C:Superfamily: common tobacco sucrose transport protein

Query Match 10.7%; Score 305.5; DB 2; Length 501;

Best Local Similarity 21.6%; Pred. No. 2.3e-15;

Matches 124; Conservative 91; Mismatches 213; Indels 145; Gaps 14;

QY 18 LLLVNLTLFGLVCLAAGITYVPPLLLEVGVBEKFMVTLGIGPVGLVCVPLLSASDH 77
Db 30 LLRVASVACGIQFGWALQSLTTPYVQLGIPHANSSIIWLGCPLSGLLVQPIVGHMSDQ 89
QY 78 WRGYRRRPPFTWALSGLILLSLFLIPRAGWAGLL--CPDPRPLELAILILGVGLLDFC 135
Db 90 CTSKYRRRPPFVAGGTAILAVIIIAHSADIGLLGDTADNKMTAIVAFVIGFWILDVA 149
QY 136 GOVCFPTPLEALLSDLF-RDPDHCROAVSVYAFMISLGGCIGYLLPAIDWDTSALAPV 194
Db 150 NMTGQPCRALLDATGNDARRTRVANAYPSLFMAIGNVLGY-----ATGAYSGW 199
QY 195 QBECLFGLTLIFLTC-----VAATLLVAEEAAL-----GPTPEAEG 232
Db 200 YKVFPPSLTSSCTINCANLKSIFYIDIIFIITVYISAAKERPRISSODGQFSEDTG 259
QY 233 SAPSLSPHCCPCRARLAFRNLGALLPRLHOLCCRMPTLRLRLFAELCSMMALMTFLFY 292
Db 260 AQ---SGHI-----EEAFLWELFGTFRLLPGSVVIVLLVTLCLNMGWFFPFL 305
QY 293 TDFVCEGLYGVPRAPSGTEARRHYDEGVNMGSLGLFLQCAISLVFSLVMDRLVQRF 352
Db 306 TDMGREIYGGEP-----NOGQSYSDGVNRGAFGMNNSVVLGITSVLMLEKLCRWGSG 359
QY 353 AVYLASVAAPFVAAAGATCLSHSVAVVYASAAITGFTFSALQILPYTLASLYHREK 412
Db 360 FWM-----GLSNLMTICFFAMLLITFTAKNDY----- 388
QY 413 KYRGDTGGASSEDLSMTSFLPGPKGAPFPNGHVGAGSGGLLPPPPALCASACDVSV 472

Db 389 -----GTNPPN---GIVISALIVPA 406
Qy 473 VVGEPTARV-VP-----GRGICLDAILDSAFLLSQVAPSPFMGSIVQL----- 516
Db 407 ILGIPLAITYSYPYALVSTRIESLGLGQGLSMGVNLAIWVPQVIVSLSGPQWDLFGGG 466
Qy 517 -SQSVTAYMWSAAGLGLVAIYFATQVVFQKSDL 548
Db 467 NSPAFVVAALSFAAGLIAAIRPRVDKSL 499

RESULT 11
S48788
sucrose transport protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S48788
R:Bueckle, X.Y.Z.; Frommer, W.B.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48788
A:Accession: S48788
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <BUE>
A:Cross-references: UNIPROT:Q40167; UNIPARC:UPI00001794EA; EMBL:X82275
C:Superfamily: common tobacco sucrose transporter protein

Query Match 10.4%; Score 297.5; DB 2; Length 428;
Best Local Similarity 25.8%; Pred. No. 7.8e-15;
Matches 114; Conservative 82; Mismatches 163; Indels 83; Gaps 18;
Qy 4 RLWWSLLRHRKAQLLLNLTFTGLEVCLAAAGITYVPPLLLEGVVEEKFTWVLGPGVL 63
Db 25 KLV-----KIIVASIAAGVQFGWALQSLTTPYVQLLGIPHRFASFVWLCPGIS 74
Qy 64 GLVCPVLGSGASDHGRYRRPFIWALSGLTLLSLFLIPRAGWLAGLLCPDP-----R 118
Db 75 GMTVPVGVGYSDNCSSRFGRRRPFIAGALVTIAVFLIGFADLI-GHASGDPLKGSK 133
Qy 119 PLEALLILGVLGDLFCQGVCTFPLEALLSDLFRDPD-HCRQAYSIVAFMISLGGCLGY- 176
Db 134 PRAIAVVGFWILDVANMLQGPCRALLADLSGGKSGKMRRTANAFSPFKAVGNILGYA 193
Qy 177 -----LLPAIDWD-TSALAPYLGTQECFL-GLLTILILFTCVAAATLL-----VAEEAALG 224
Db 194 AGSYSRLFKVFPFSKTKACDMYRANLKSCFFIAIFLLLSLTLLTALTLVRENELPEKEELE 253
Qy 225 PTEPAEGLSAPLSPHCCPCRARLAFRNLGALLPRLHQLCCMRPRTLRLRFVAELCSWMA 284
Db 254 IDEKLSGAG-----KSKVFP--FGEIFGALKDL-----PRPMWILLVTCNLWIA 296
Qy 285 LMTFTLFTYDFVGEGLYQGVPRAPGTEARRHYDEGVRMGSLGFLTQCAISLVFSLVMDR 344
Db 297 WFPFFLYDTDMAKEVFGG---QVGD--AKLYDLGVRAGALGQLLSVVLGFMWSLGVF 350
Qy 345 LVORFGTRAVYLASVAFVPAAGATCLSHSVAVV-----TASAAATGFT----- 388
Db 351 LGRKIG-GAKRLWGLNFVL---AICLAMTILTVKMAEKSRRGHDAAGTLMGTPPGVKIGA 406
Qy 389 ---FSALQI-----LPYTLA 400
Db 407 LLLFAALGICPLAVTFSIPFALA 428

RESULT 12
S38657
sucrose transport protein ptpl - common plantain
N:Alternate names: sucrose transporter ptpl
C:Species: Plantago major (common plantain)
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S38657
R:Gahrtz, M.; Stolz, J.; Sauer, N.
submitted to the EMBL Data Library, November 1993

A:Reference number: S38657
A:Accession: S38657
A:Molecule type: mRNA
A:Residues: 1-510 <GAH>
C:Cross-references: UNIPROT:Q40938; UNIPARC:UPI00000A55AF; EMBL:X75764; NID:G415987; PI1
C:Genetics:
A:Gene: ptpl
C:Superfamily: common tobacco sucrose transporter protein
C:Keywords: sugar transport
Query Match 10.3%; Score 294; DB 2; Length 510;
Best Local Similarity 24.7%; Pred. No. 1.7e-14;
Matches 126; Conservative 77; Mismatches 199; Indels 108; Gaps 19;
Qy 18 LLLVNLTLFTGLEVCLAAAGITYVPPLLLEGVVEEKFTWVLGIPVLGVCVPLLGASDPH 77
Db 29 IFLVAAIAAGVQFGWALQSLTTPYVQLLGIPHKWASYIWLCPGISGMIVQVPVGFSDN 88
Qy 78 WRGRYRRRPFIWALSGLTLLSLFLIPRAGWLAGL-----LCPDRPRLLEALLILGV 129
Db 89 CTSRFGRRRPFI-AGAGLGVAVVLI---GFAADLGHAGGDSLGDGLKPRAGVVFVGF 144
Qy 130 GLLDFCGQVCTFPLEALLSDLF-RDPDHCQRQAYSIVAFMISLGGCLGYLLPAID----- 182
Db 145 WILDVANMLQGPCRALLADLSGGNTKMANANSFSPFMAYGNVLGYAAGSYSRMYKV 204
Qy 183 --WDTSALAPYLGTQEC-LFGLLTILFTCVAAATLL-----VAEEAALGPTPEAELSA 234
Db 205 PFSKTKACDIYCANUKSCFIISITLITLITLUALSIVREKRVAAEQV---TAACKGFPI 261
Qy 235 PSLSPHCCPCRARLAFRNLGALLPRLHQLCCMRPRTLRLRFVAELCSMMALMTFTLYTD 294
Db 262 P-----VFPELFGALKDLPRPMWILLVLTALNIAWFGFLIFD 301
Qy 295 FVGEGLYQGVPRAPGTEARRHYDEGVRMGSLGFLTQCAISLVFSLVMDRLVQREG---- 350
Db 302 WNGREYV-GETQCHKAPELAVIYNGVSAAGALGLMLNSIVLGFASLGVOYMARALGVK 360
Qy 351 -----TFAVVLA-SVAAPVPAAGATCLSHSVAVVTAALTG--FTFSALQI----- 394
Db 361 LMGVNFILAIICMTIVITVKASHRYPYNSGVLTQTPSSVKIGALVFSALGIPLAITF 420
Qy 395 -LPYTLASLYHREKQVFLPKYRGDTGGASSEDLSL-----MTSFLPGKPG---- 438
Db 421 SVFPFALASIIY-----STTTGSGQLSLGVNLAIVIPQMIIVSVASGPMDFG 468
Qy 439 ----APFPNGHVAGGSG-----LLPPPPA 459
Db 469 GGNLPAFVVGAVAAAAAGSIFAFMTLPSPPPA 498

RESULT 13
S51114
sucrose-proton symporter - beet
C:Species: Beta vulgaris (beet)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51114
R:Westram, A.; Eckhardt, U.; Frommer, W.B.; Riesmeier, J.W.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence of a sugar beet sucrose transporter cDNA.
A:Reference number: S51114
A:Accession: S51114
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <WES>
A:Cross-references: UNIPROT:Q39438; UNIPARC:UPI00000A55B7; EMBL:X83850; NID:G633171; PI1
C:Superfamily: common tobacco sucrose transporter protein

Query Match 10.3%; Score 294; DB 2; Length 523;
Best Local Similarity 24.3%; Pred. No. 1.8e-14;
Matches 125; Conservative 78; Mismatches 199; Indels 112; Gaps 20;
Qy 17 QLLVNLTLFTGLEVCLAAAGITYVPPLLLEGVVEEKFTWVLGIPVLGVCVPLLGASD 76

Db 38 KLAIVASIAAGVQFGWALQSLTTPYVQLLGIPTHTWAPIYIWLCPISGMIVQPTGVYSD 97
QY 77 HWRGRYRRRPFTHWALSLGILLSLFLIPRAGMLA--GLLCPD-----PRLELALLILGV 129
Db 98 RCTSKGRRRPFTHWALSLGILLSLFLIPRAGMLA--GLLCPD-----PRLELALLILGV 154
QY 130 GLLDGFCQVQFTPLEALLSLDFRDPD--HCRQAVSVYAFMISLGGCLGY-----LLP 179
Db 155 WILDVANNTLQGPCRALLADMAAGSQAKRYANAFSFFMALNIGGAGSYGRLYTVFP 214
QY 180 AIDWDTSAAPYLGTOBECLFGLLTFLITCVAAATLLVAEEAALGPTPEAGLSAPSLSP 239
Db 215 FT--HTKACDTCYCANLKSCEFFITLLVLTILALSVRER---PFTLEIOEEENLKN 268
QY 240 HCCPCRLARLAFNLGALLPRLHOLCCMRPRTLRLFAELCSNMALMTFTFLYDFVGE 299
Db 269 NTGGC--ARLPF--FGQLFGALKOL---PKMLILLVTCNLNIAFPFLFOTDMWGRE 321
QY 300 LYQGVPAEPTGEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQVREG--TRAVYLA 357
Db 322 VYGGT-----VGEGRAYDMGVHAGALGLMINSVLGINSLGIEKLARLVGGVYKRLWIV 375
QY 358 SVAAPFVAAGATCLSHSAVVTTASA-----ALTGF 387
Db 376 NLIL-----AVCLAMTI-LVTKSAEYRATHVPGAIGPPPLPPGVKGGALAIFAVLGI 428
QY 388 TFSALQILPYTLASLYHREK-----QVFLPKYRGDTGASSEDLSMT 429
Db 429 PLAITSIPPALASIFSASGSGOGLSLGVNLAIIVPQMFVSVTSGPW-----DAL-- 480
QY 430 SPLPGPKGAPFPNGHVHAGCGSG-----LLPPPP 458
Db 481 -FGGNLPA--FVUGAVAATASAILSLFTLLPPPP 511

RESULT 14

F96741
probable sucrose transport protein F17M19.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96741
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: UNIPROT:Q9C8X2; UNIPARC:UPI0000048458; GB:AE005173; NID:g6978914; P1
C;Genetics:
A;Gene: F17M19.4
A;Map position: 1
C;Superfamily: common tobacco sucrose transport protein

Query Match 10.2%; Score 292.5; DB 2; Length 512;
Best Local Similarity 23.8%; Pred. No. 2.2e-14;
Matches 120; Conservative 87; Mismatches 211; Indels 87; Gaps 18;
QY 17 QLLLVNLLTFGLVCLAAAGTIVVPPLLLEVGVEEKFMTVMVLGIGPVGLVVCVPLLSASD 76
Db 33 KIISVASIAAGVQFGWALQSLTTPYIQLLGIPTHTWAPIYIWLCPISGMIVQPTGVYSD 92
QY 77 HWRGRYRRRPFTHWALSLGILLSLFLIPRAGMLA--GLLCPD-----PRLELALLILGV 129

Db 93 RCESREGRRRPFTHWALSLGILLSLFLIPRAGMLA--GLLCPD-----PRLELALLILGV 149
QY 130 GLLDGFCQVQFTPLEALLSLDFRDPD--HCRQAVSVYAFMISLGGCLGY-----LL 178
Db 150 WILDVANNTLQGPCRALLADMAAGSQAKRYANAFSFFMALNIGGAGSYGRLYTVFP 209
QY 179 PAIDWDTSAAPYLGTOBECLFGLLTFLITCVAAATLLVAEEAALGPTPEAGLSAPSLSP 238
Db 210 PFT--MTKACDIYCANLKSCEFFITLLVLTILALSVRER---PFTLEIOEEENLKN 263
QY 239 PHCCPCRLARLAFNLGALLPRLHOLCCMRPRTLRLFAELCSNMALMTFTFLYDFVGE 298
Db 264 -----SLFF--FGEIFGAVR---HMKRPMVMLLITVINIAFWPFILYDITDMGR 309
QY 299 GLYQGVPAEPTGEARRHYDEGRVMSGLGLFLOCAISLVFSLVMDRLVQVREG--TRAVYLA 358
Db 310 EYVGG--NSDGDERSKLYDQGVQAGALGLMINSVLGINSLGIEKLARLVGGVYKRLWIV 366
QY 359 VAAFPVAAGATCLSHSAVVTTASA-----SAALTGFTTFSALQIL 395
Db 367 CVNFILAIG---LAMTVLTKSAEYRATHVPGAIGPPPLPPGVKGGALAIFAVLGI 423
QY 396 -PYTLASLYHREKQVFLPKYRGDTGASSEDLSMTSFLPGKP-----GAPFPN---GHVG 447
Db 424 IPFALASIFSTNSGAGCGGLSLGVNLAIIVPQMFVSVTSGPW-----DAL-- 483
QY 448 AGSGGLL-----PPP--PALCGA 463
Db 484 AAVSGVLAITVLPSPPPDAPAMSGA 508

RESULT 15

T02982
probable sucrose transport protein - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02982
R;Hirose, T.; Imaiizumi, N.; Scofield, G.N.; Furbank, R.T.; Ohsugi, R.
Plant Cell Physiol. 38, 1389-1396, 1997
A;Title: cDNA cloning and tissue specific expression of a gene for sucrose transporter
A;Reference number: Z14809; MUID:98182940; PMID:9522469
A;Accession: T02982
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-537 <HIR>
A;Cross-references: UNIPROT:O49838; UNIPARC:UPI00000A2688; EMBL:D87819; NID:g2723470; P
A;Experimental source: cultivar Nipponbare, leaf
C;Genetics:
A;Gene: SUT1
C;Superfamily: common tobacco sucrose transport protein

Query Match 10.2%; Score 292; DB 2; Length 537;
Best Local Similarity 26.7%; Pred. No. 2.6e-14;
Matches 115; Conservative 72; Mismatches 167; Indels 76; Gaps 19;
QY 17 QLLLVNLLTFGLVCLAAAGTIVVPPLLLEVGVEEKFMTVMVLGIGPVGLVVCVPLLSASD 76
Db 51 RUIISGVAVAGVQYQWALQSLTTPYVQTLGLSHALTSFMWLCGPIAGWVQVCVGLYSD 110
QY 77 HWRGRYRRRPFTHWALSLGILLSLFLI---PRAGWLAGLLCPD-----PRLELALLIL 127
Db 111 RCTSKWRRRPYILTGCVLICLAVVVGFSADIGYAMGDTKEDCSYVHSGRMAAIVVYL 170
QY 128 GVCLLDPCQVCFPTLEALLSLDF--RDPDHCRAQVSVYAFMISLGGCLGYLLPAID--- 182
Db 171 GFWLLDFSNNTVOGPARALMADLSGRHFGP---TANSIFCSNMWMLNIGYSSGSTNNWH 227
QY 183 -WDTSAAPYLGTOBECLFGLLTFLITCVAAATLLVAEEAALGPTPEAGLSAPSLSP 226
Db 228 KW-----FPFLKTRACCEACANLKGAFVAVIFLSLCLVITLIFAKEVFPGKNAAL-PTK 281
QY 227 --EPAGELSAPSLPHCCPCRLARLAFNLGALLPRLHOLCCMRPRTLRLFAELCSNMA 284

Db 282 SNEPAEPECTG-----PLAVLKGFRNLPTCMPSV-----LIVTGL-TWLS 320
QY 285 LMTFTLFYTDYFVGEGLYQGVPR-AEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMD 343
Db 321 WFFFLYDIDWNGREIYHGDPKGTDPOIEA---FNGQVRAGAGLLNSIVLGFSSFLIE 377
QY 344 RLVRFGTTRAVYLASVAAPFVAAGATCL-----SHSVA--VVTASAAALTGFTFSALQ 393
Db 378 PNCRKVGPRVWVTSNFLVCIAAATALI SFWSLKDHFHCTVOKAITADKSIKAVCLVLFA 437
QY 394 ILPYTLASLY 403
Db 438 FLGVPLAVLY 447

Search completed: May 27, 2006, 04:05:32
Job time : 45 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 03:56:28 ; Search time 302 Seconds
(without alignments)
1693.820 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLRRHKAQLLL.....AIYFATQVVFDKSLAKYSA 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2861	100.0	553	1 S45A3_HUMAN	Q96Jt2 homo sapien
2	2798	97.8	553	1 S45A3_MACFA	Q95K15 macaca fasc
3	2602	90.9	553	1 S45A3_MOUSE	Q8k0h7 mus musculus
4	1375	48.1	578	2 Q4SKH1_TETNG	Q4skel tetraodon n
5	1366	47.7	550	2 Q6PCJ2_BRARE	Q6pcj2 brachydanio
6	1291	45.1	560	2 Q6PCJ0_XENLA	Q6pcj0 xenopus lae
7	1156	40.4	231	2 Q658X7_HUMAN	Q658x7 homo sapien
8	621	21.7	555	2 Q7Q8T1_ANOGA	Q7q8t1 anopheles g
9	567.5	19.8	618	2 Q6NL41_DROME	Q6nl41 drosophila
10	519.5	18.2	599	2 Q9VSV1_DROME	Q9vsv1 drosophila
11	491	17.2	675	2 Q4R136_TETNG	Q4r136 tetraodon n
12	489.5	17.1	530	1 S45A2_MOUSE	P58J55 mus musculus
13	489.5	17.1	530	2 Q541S3_MOUSE	Q541s3 mus musculus
14	488.5	17.1	530	1 S45A2_HUMAN	Q9unx9 homo sapien
15	488.5	17.1	614	2 Q7Q8Q4_ANOGA	Q7q8q4 anopheles g
16	487	17.0	569	2 Q4SQA7_TETNG	Q4sqa7 tetraodon n
17	486.5	17.0	532	2 Q4L888_PIG	Q4l888 sus scrofa
18	484.5	16.9	530	2 Q8C204_MOUSE	Q8c204 mus musculus
19	477.5	16.7	548	2 Q566F3_XENLA	Q566f3 xenopus lae
20	471	16.5	549	2 Q5M7S3_XENTR	Q5m7s3 xenopus tro
21	469.5	16.4	460	2 Q6P2P0_HUMAN	Q6p2p0 homo sapien
22	466	16.3	804	2 Q4RX49_TETNG	Q4rx49 tetraodon n
23	457.5	16.0	782	1 S45A1_HUMAN	Q9y2w3 homo sapien
24	456	15.9	576	2 Q90274_ORYLA	Q90274 oryza lat
25	455	15.9	751	1 Q566E3_RAT	Q566e3 rattus norv
26	451	15.8	751	1 S45A1_MOUSE	Q8bi77 mus musculus
27	449.5	15.7	529	2 Q2PUG5_CANFA	Q2pug5 canis famil
28	446	15.6	751	1 S45A1_FAT	Q8k4s3 rattus norv
29	436	15.2	785	2 Q3V0B8_MOUSE	Q3v0b8 mus musculus
30	434	15.2	521	2 Q7Q8Q7_ANOGA	Q7q8q7 anopheles g
31	431	15.1	425	2 Q7Q8Q6_ANOGA	Q7q8q6 anopheles g

32	415	14.5	740	2 Q5BKX6_HUMAN	Q5bkx6 homo sapien
33	415	14.5	798	2 Q6ZRI2_HUMAN	Q6zri2 homo sapien
34	396.5	13.9	429	2 Q5TLW0_9CICH	Q5tlw0 neolamprolo
35	396	13.8	720	2 Q6PDG3_MOUSE	Q6pdg3 mus musculus
36	394.5	13.8	754	2 Q7KWK4_DICDI	Q7kwk4 dictyosteli
37	391.5	13.7	429	2 Q5TLW1_9CICH	Q5tlw1 lamprologus
38	391.5	13.7	429	2 Q5TLW4_ALTCL	Q5tlw4 altolamprol
39	390.5	13.6	429	2 Q5TLW2_9CICH	Q5tlw2 astatotilap
40	387.5	13.5	429	2 Q5TLW3_9CICH	Q5tlw3 autonocara
41	378	13.2	460	2 Q7Q8Q5_ANOGA	Q7q8q5 anopheles g
42	369.5	12.9	2176	2 Q4SJ20_TETNG	Q4sj20 tetraodon n
43	347.5	12.1	515	2 Q6S803_DAUCA	Q6s803 daucus caro
44	347.5	12.1	515	2 Q9FNR6_DAUCA	Q9fnr6 daucus caro
45	346.5	12.1	501	2 Q9SQK6_VITVI	Q9sqk6 vitis vinif

ALIGNMENTS

RESULT 1
S45A3_HUMAN
ID S45A3_HUMAN STANDARD; PRT; 553 AA.
AC Q96JT2;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Solute carrier family 45 member 3 (Prostate cancer-associated protein
DE 6) (Protein).
DE Name=SUC45A3; Synonyms=PCANAP6, PRST;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Prostate;
RX MEDLINE=21139094; PubMed=11245466;
RA Xu J., Kalos M., Stolk J.A., Zasloff E.J., Zhang X., Houghton R.L.,
RA Filho A.M., Nolasco M., Badaro R., Reed S.G.;
RA "Identification and characterization of prostein, a novel prostate-
specific protein.";
RA Cancer Res. 61:1563-1568 (2001).
RL [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=PNS;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Roshlyuk S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP TISSUE SPECIFICITY.
RX PubMed=14957204; DOI=10.1038/sj.bjc.6601642;
RA Kieselring A., Stevanovic S., Fuessel S., Weigle B., Rieger M.A.,
RA Temme A., Rieber E.P., Schmitz M.;
RA "Identification of an HLA-A(*)0201-restricted T-cell epitope derived

from the prostate cancer-associated protein prostein.";
Br. J. Cancer 90:1034-1040(2004).
-|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (Potential).
-|- TISSUE SPECIFICITY: Prostate-specific. Expressed in all prostatic glandular cells. Expressed both in normal and cancerous prostates.
-|- INDUCTION: Up-regulated by androgens.
-|- MISCELLANEOUS: Marker for prostate cells. May be used, in case of prostate cancers, as a target antigen for prostate carcinomas-directed cytotoxic T-cell lymphocytes.
-|- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH) cation symporter transporter (TC 2.A.2) family.

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EMBL: AY033593; AAK54386.1; -; mRNA.
EMBL: BC050416; AAH50416.1; -; mRNA.
Ensembl: ENSG00000158715; Homo sapiens.
HGNC: HGNC:8642; SLC45A3.
MIM: 605097; Gene.
MIM: 608319; Gene.
InterPro: IPR011701; MFS_1.
Pfam: PF07690; MFS_1; 1.
Membrane; Transmembrane; Transport.
Solute carrier family 45 member 3.
/FTid=PRO_0000122519.
CHAIN 1 553
TRANSMEM 19 39
TRANSMEM 52 72
TRANSMEM 88 108
TRANSMEM 120 140
TRANSMEM 161 181
TRANSMEM 198 218
TRANSMEM 275 295
TRANSMEM 323 343
TRANSMEM 353 373
TRANSMEM 382 402
TRANSMEM 522 542
TRANSMEM 545 458
COMPTAS 553 553
SEQUENCE 553 AA; 59323 MW; 0AFA23FBC742A667 CRC64;
Query Match 100.0%; Score 2861; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.7e-210; Mismatches 0; Indels 0; Gaps 0;
Matches 553; Conservative 0;
1 MVQRLVWSRLRHRKAQLLLVNLITFGLVCLAAAGITVVPPLLEVGVGEKFTMWLGIG 60
1 MVQRLVWSRLRHRKAQLLLVNLITFGLVCLAAAGITVVPPLLEVGVGEKFTMWLGIG 60
61 PVLGLVCPVLLGSADHWGRGRRRPFIALSLGILLISLFLIPRAGWLAGLCPDRPL 120
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121 ELALLILVGLLDFCGQVCFPLEALLSDLPDCHCRQAYSVAFMISLGGCLGYLLPA 180
121 ELALLILVGLLDFCGQVCFPLEALLSDLPDCHCRQAYSVAFMISLGGCLGYLLPA 180
181 IDWDTLSALAPYLGTOECLFGLLTILFTCVAAATLLVAEEAALGTEPAEGLSAPLSPH 240
181 IDWDTLSALAPYLGTOECLFGLLTILFTCVAAATLLVAEEAALGTEPAEGLSAPLSPH 240
241 CCPCRARLAFNLGALLPRLHQLCCMRPTRLRLFVAELCSWMAWMTTFLYTFDVGEG 300
241 CCPCRARLAFNLGALLPRLHQLCCMRPTRLRLFVAELCSWMAWMTTFLYTFDVGEG 300
301 YQGVPAEPTGTEARRHYDEGVGMGLFLQCAISLVFSLVMDRLVQRFGRVAVLASVA 360
301 YQGVPAEPTGTEARRHYDEGVGMGLFLQCAISLVFSLVMDRLVQRFGRVAVLASVA 360
361 APVAAAGATCLSHSVAVVTASALTGFTESALQILPYTLASLYHREKQVFLPKYRGDTGG 420
361 APVAAAGATCLSHSVAVVTASALTGFTESALQILPYTLASLYHREKQVFLPKYRGDTGG 420

421 ASSEDSLMTSFLPGPKGAPPFNHGVGAGSGLLPPBALCGASACDVSVRVVVGPEA 480
421 ASSEDSLMTSFLPGPKGAPPFNHGVGAGSGLLPPBALCGASACDVSVRVVVGPEA 480
481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYPATQ 540
481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGISVQLSQSVTAYMVSAAGLGLVAIYPATQ 540
541 VVFDKSLAKYSA 553
541 VVFDKSLAKYSA 553

RESULT 2
S45A3 MACFA STANDARD; PRT; 553 AA.
ID S45A3 MACFA
AC Q95KI5; Q95KC5;
DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Solute carrier family 45 member 3 (Prostate cancer-associated protein 6) (Protein).
DE Name=SLC45A3; Synonyms=PCANAP6, PRST; ORFNames=QmOA-10594, Qcra-11310;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopitheciinae; Macaca.
OC NCBI_taxid=9541;
OX [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Medulla oblongata, and Temporal cortex;
RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH) cation symporter transporter (TC 2.A.2) family.

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EMBL: AB060851; BAB46871.1; -; mRNA.
EMBL: AB062977; BAB60745.1; ALT_INIT; mRNA.
InterPro: IPR011701; MFS_1.
Pfam: PF07690; MFS_1; 1.
Membrane; Transmembrane; Transport.
Solute carrier family 45 member 3.
/FTid=PRO_0000122520.
CHAIN 1 553
TRANSMEM 19 39
TRANSMEM 52 72
TRANSMEM 88 108
TRANSMEM 120 140
TRANSMEM 161 181
TRANSMEM 198 218
TRANSMEM 275 295
TRANSMEM 323 343
TRANSMEM 353 373
TRANSMEM 382 402
TRANSMEM 522 542
TRANSMEM 545 458
COMPTAS 553 553
SEQUENCE 553 AA; 59393 MW; 0718F3A91FB3BF1E CRC64;
Query Match 97.8%; Score 2798; DB 1; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.2e-205; Mismatches 2; Indels 0; Gaps 0;
Matches 542; Conservative 2;
1 MVQRLVWSRLRHRKAQLLLVNLITFGLVCLAAAGITVVPPLLEVGVGEKFTMWLGIG 60

Db 1 MVQRLVSVRLRRKRAQLLLINLLTFGLVCLAAAGITYVPPPLLLVGVBEKEFTWVLGIG 60
 QY 61 PVGLGVCVPLGASDHWRGRRPFFTWLSLGLTLLSLFLTPRAGWLAGLLCPDPRPL 120
 Db 61 PVGLGVCVPLGASDHWRGRRPFFTWLSLGLTLLSLFLTPRAGWLAGLLCPDPRPL 120
 QY 121 ELALLIGVGLDFGCGVCFPTPLLEALLSDFDPDRCRQAYSAYAFMISLGGCGLYLLPA 180
 Db 121 ELALLIGVGLDFGCGVCFPTPLLEALLSDFDPDRCRQAYSAYAFMISLGGCGLYLLPA 180
 QY 181 IDWDTSAALPYLGTQECFLGTLTLFLTCVAATLVAAEALGPTPEAGLSAPLSLPH 240
 Db 181 IDWDTSAALPYLGTQECFLGTLTLFLTCVAATLVAAEALGPTPEAGLSAPLSLPH 240
 QY 241 CPCPCARLARFRNLGALLPRHLQCCMRPTLRFLFAELCSWMLMTFTFLFYTDFFVGEGL 300
 Db 241 CPCPCARLARFRNLGALLPRHLQCCMRPTLRFLFAELCSWMLMTFTFLFYTDFFVGEGL 300
 QY 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLQCAISLVFLVMDRLVORFGTRAVYLASVA 360
 Db 301 YQGVPRAEPTGEARRHYDEGRVMSGLGLFLQCAISLVFLVMDRLVORFGTRAVYLASVA 360
 QY 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
 Db 361 APVAAAGATCLSHSVAVVTASAAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
 QY 421 ASSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
 Db 421 TSSEDSLMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
 QY 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAGLGLVAVFYATQ 540
 Db 481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMSGIVQLSQSVTAYMVSAAGLGLVAVFYATQ 540
 QY 541 VVFDKSDLAKEYS 552
 Db 541 VVFDKSDLAKEYS 552

RESULT 3
 ID S45A3 MOUSE STANDARD; PRT; 553 AA.
 AC Q8KH07; Q8K252; Q8R110;
 DT 13-APR-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Solute carrier family 45 member 3 (prostate cancer-associated protein 6) (Protein).
 DE Name=Slc45a3; Synonyms=Pcanap6, Prst;
 GN Mus musculus (Mouse).
 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.B., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel G., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Fabriz S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reid J., Ring J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K., Tamao J.K., Tan S.-L., Tang S., Taylor R., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RN Science 309:1559-1563 (2005).
 RL [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Colon, Liver, and Mammary tumor;
 RX MEDLINE=2238257; PubMed=12477912; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [3]
 RN TISSUE SPECIFICITY.
 RP PubMed=14561649; DOI=10.1095/biolreprod.103.021493;
 RX Hsia N., Cornwall G.A.;
 RA "DNA microarray analysis of region-specific gene expression in the mouse epididymis.";
 RT Biol. Reprod. 70:448-457 (2004).
 RL CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (Potential).
 CC CC -!- TISSUE SPECIFICITY: Expressed in the epididymis.
 CC CC -!- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH) cation symporter transporter (TC 2.A.2) family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC -----
 CC EMBL: AK035428; BAC29063.1; -; mRNA.
 DR EMBL: BC024519; AAH24519.1; -; mRNA.
 DR EMBL: BC031381; AAH31381.1; -; mRNA.
 DR EMBL: BC034084; AAH34084.1; -; mRNA.
 CC Ensembl: ENSMUSG0000026435; Mus musculus.
 DR MGI: MGI:1922082; Slc45a3.
 DR GO: GO:0016021; C-integral to membrane; TAS.
 DR InterPro: IPR011701; MFS_1.
 DR Pfam: PF07690; MFS_1.

KW	Membrane; Transmembrane; Transport.	
FT	CHAIN	1 553
FT		/FTId=PRO 0000122521.
FT	TRANSMEM	19 39
FT	TRANSMEM	52 72
FT	TRANSMEM	88 108
FT	TRANSMEM	120 140
FT	TRANSMEM	161 181
FT	TRANSMEM	198 218
FT	TRANSMEM	275 295
FT	TRANSMEM	323 343
FT	TRANSMEM	353 373
FT	TRANSMEM	382 402
FT	TRANSMEM	522 542
SEQ	SEQUENCE	553 AA; 59742 MW; 6A474FEA630B4B13 CRC64;
Query Match		
Best Local Similarity 90.9%; Score 2602; DB 1; Length 553;		
Matches 502; Conservative 14; Mismatches 36; Indels 0; Gaps 0;		
QY	1	MVORLWVSRLLRRKKAQLLVNLLTFGLEVCLAAAGITYVPPLLLEVGVEEKFTMTVLGIG 60
Db	1	MIQRLWASRLRRKKAQLLVNLLTFGLEVCLAAAGITYVPPLLLEVGVEEKFTMTVLGIG 60
QY	61	PVLGLVCPVLLGSASDHRGRYGRRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDPRPL 120
Db	61	PVLGLVSPVLLGSASDQWRGRYGRRRPFIWALSGLVLLSLFLIPRAGWLAGLLPDPTRPL 120
QY	121	ELALLIGVGLDFCGQVCTPRLALLSLDFRDPDHCROQYSVYAFMISLGGCLGYLLPA 180
Db	121	ELALLIGVGLDFCGQVCTPRLALLSLDFRDPDHCROQYSVYAFMISLGGCLGYLLPA 180
QY	181	IDWDTSAALPYLGTQEBCLFGLTLTFLTCVAATLLVAEEAALGPTPEAGLSAPLSPH 240
Db	181	IDWDTSVIAPYLTQEBCLFGLTLTFLTCMAATLFTVEEAVLGPPPEAGLLVSVSR 240
QY	241	CCPCRLARLAFNIGALLPRHQJCCRMPTLRFLFVAELCSWALMTFTLYTDFVGEGL 300
Db	241	CCPCHVGLAFNIGTLTPRLQJCCRMPTLRFLFVAELCSWALMTFTLYTDFVGEGL 300
QY	301	YQGVPRAPGTEARRHHYDEGVRMGSLGLFQCAISLVFSLVMDRLVQRFOTRAVYLASVA 360
Db	301	YQGVPRAPGTEARRHHYDEGIRMGSLGLFQCAISLVFSLVMDRLVQKFGTRSYLASVM 360
QY	361	AFVPAAGATCLSHSVAVVTASALTGTFTSALQILPYTLASLVHREKQVFLPKYRGDTGG 420
Db	361	TFVAAAATCLSHSVVVVVTASALTGTFTSALQILPYTLASLVHREKQVFLPKYRGDAGG 420
QY	421	ASSEDLSMTSFLPGPKGAPFNGHVGAGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
Db	421	SSGEDSQTTSLPGPKGALFPNGHVGSGSGGILAPPPALCGASACDVSMRVVVGEPPEA 480
QY	481	RVVPGRGICDLAILDGAFLLSQVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYPATQ 540
Db	481	RVTGREGICDLAILDGAFLLSQVAPSLFMGSIQVLSHVSITAYMVSAAGLGLVAIYPATQ 540
QY	541	VVFDKNDLAKYS 552
Db	541	VVFDKNDLAKYS 552
RESULT 4		
Q4SKE1_TETNG PRELIMINARY; PRT; 578 AA.		
AC	Q4SKE1	
DT	19-JUL-2005, integrated into UniProtKB/TREMBL.	
DT	19-JUL-2005, sequence version 1.	
DE	Chromosome 13 SCAP14566; whole genome shotgun sequence. (Fragment).	
GN	TrFNAMES=GSTENG00016776001.	
OS	Tetraodon nigroviridis (Green puffer).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	

RC	TISSUE=Embryo;	DE	Hypothetical protein DKFp666D0110.
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;	GN	Name=DKFp666D0110;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,	OS	Homo sapiens (Human).
RA	Richardson P.,	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus	OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
RT	initiative."	OC	Homo.
RL	Dev. Dyn. 225:384-391 (2002).	OX	NCBI_TaxID=9606;
RN	[3]	RN	[1]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Embryo;	RC	TISSUE=Stomach;
RA	Klein S., Strausberg R.,	RG	The German cDNA Consortium;
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.	RA	Ansoerge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	RA	Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
CC	Distributed under the Creative Commons Attribution-NoDerivs License	RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC	-----	CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License	CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----	CC	-----
DR	EMBL; BC059306; AAH59306.1; -; mRNA.	DR	EMBL; AL832933; CAH56282.1; -; mRNA.
DR	InterPro; IPR011701; MFS_1.	DR	Ensembl; ENSG00000158715; Homo sapiens.
DR	Pfam; PF07690; MFS_1; 1.	KW	Hypothetical protein.
SQ	SEQUENCE 560 AA; 62717 MW; ACS26D5675AD7A10 CRC64;	SQ	SEQUENCE 231 AA; 23767 MW; DOA5A64F3107F475 CRC64;
Query Match 45.1%; Score 1291; DB 2; Length 560;		Query Match 40.4%; Score 1156; DB 2; Length 231;	
Best Local Similarity 46.6%; Pred. No. 3.4e-90;		Best Local Similarity 100.0%; Pred. No. 2.8e-80;	
Matches 267; Conservative 93; Mismatches 147; Indels 8;		Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	18 LLLVNLTLFGLVCLAGITYVPPLLLEVGVEBKFTMWLGIPVLGLVCVPLLGASDH 77	QY	323 MGSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVAAPFVAAGATCLSHSVAVVTASA 382
DB	10 LVLNFMTCGLEICVAAGITYVPPLLLEAGVERQYMTVLGIGPVLGLIFVPLIGASDN 69	DB	1 MGSGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVAAPFVAAGATCLSHSVAVVTASA 60
QY	78 WRGRYGRRPFIFWLSGILLSLFLIPRAGWLAGLLCPDRPLELALLIGVLLDFCGQ 137	QY	383 ALTGTFFSALQILPYTLASLYHREKQVFLPKYRGDTGGASDLSMTSFLPGKPGCAPPP 442
DB	70 CQSTLGRRRPFIFWLSVGVLSLFLIPHADSLASFNSREKNKHAHIFILFGVLLDCCVQ 129	DB	61 ALTGTFFSALQILPYTLASLYHREKQVFLPKYRGDTGGASDLSMTSFLPGKPGCAPPP 120
QY	138 VCTPTEALLSDLFRDPDHCQRQYSVYAFMISLGGCLGYLLPAIDWDTGALAPYLGTQBE 197	QY	443 NGHVGAGSGLLPPPPALCGASACDVSVRVVVGTEARVVPGRGICLDLALDSAFLLS 502
DB	130 VCTPTEALLSDLCHDDGCGQAFAMFSFMISFGGCGYLLTSVNNYTVISLYFGGQDE 189	DB	121 NGHVGAGSGLLPPPPALCGASACDVSVRVVVGTEARVVPGRGICLDLALDSAFLLS 180
QY	198 CLFGLLTLIFLTCVAATLLVAEE-----AALGTEPA-----EGLSAPLSPHCCPCR 245	QY	503 QVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQVVFQKSLAKYSA 553
DB	190 CLFLLLVFIISLVMTKTSSEPFYNSQORMDKPTSTGSLHRCMPKWLRSWKCN 249	DB	181 QVAPSLFMGSIQVLSQSVTAYMVSAAGLGLVAIYFATQVVFQKSLAKYSA 231
QY	246 ARLAFRNL-GALLPLRHOLCRPRLRLFLVABLCSWMAIMTFTLYTDFVGEGLYQGV 304	RESULT 8	
DB	250 PLFCLLSLCSVTPRVSSYCRIPSVNKLCAQLCSWMAVMSFMYTDFVGEGLYNGI 309	Q7QETL ANOGA PRELIMINARY; PRT; 555 AA.	
QY	305 PRAEPGTEARRHYDEGVMSGLGLFLQCAISLVFSLVMDRLVORFGTRAVYLASVAAPV 364	AC Q7QETL; 15-DEC-2003, integrated into UniProtKB/TrEMBL.	
DB	310 PSAAPGTESRLRYDEGIRMGSGILFLQCAISTFSSVIMNKLTKHFGSRRYILASWVTF 369	DT 07-FEB-2006, entry version 10.	
QY	365 AAGATCLSHSVAVVTASAALTGTFSALQILPYTLASLYHREKQVFLPK---YRGDTGGA 421	DT 07-FEB-2006, entry version 10.	
DB	370 SALVICLSQNIIVITIMSSUTGFAIATLQTLPTLCLICLHKQDVFMFRAVLSONKNGYT 429	DE ENSANGP0000008133 (Fragment).	
QY	422 SSEDLSMTS-----FLPGP---KPGAPFPNGHVAGGSGLLP 455	GN CRFNames=ENSANGG0000006137;	
DB	430 LTKEAIVFSSNNEDGTFKNGAPQGEKHIYIPHELETYTQDVPYPS-----NSILP 482	OC Anopheles gambiae str. PEST.	
QY	456 PPPALCGASACDVSVRVVVGTEARVVPGRGICLDLALDSAFLLSQVAPSLFMGSI 515	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
DB	483 -----AVOKETSQDNYTQRGIGLDFATLDSAFLLSQVFPFPMGMIVQ 525	OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;	
QY	516 LSQSVTAYMVSAAGLGLVAIYFATQVVFQKSDL 548	OC Anophelinae; Anopheles.	
DB	526 FMENVTVIASSVLFGVFAIYILASRVVFDQKDL 558	OX NCBI_TaxID=180454;	
RESULT 7		[1]	
Q658X7_HUMAN PRELIMINARY; PRT; 231 AA.		NUCLEOTIDE SEQUENCE.	
AC Q658X7; 25-OCT-2004, integrated into UniProtKB/TrEMBL.		The Anopheles gambiae Sequence Committee;	
DT 25-OCT-2004, sequence version 1.		The Anopheles gambiae re-annotation."	
DT 07-FEB-2006, entry version 7.		Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	
-----		[2]	
-----		NUCLEOTIDE SEQUENCE.	
-----		The Anopheles gambiae Sequence Committee;	
-----		Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.	
-----		-!- CAUTION: The sequence shown here is derived from an	
-----		EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is	
-----		preliminary data.	
-----		-----	

OC Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea: Drosophilidae; Drosophila.
OX NCBI_TaxID=727;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX ADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,
RA Ballew R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle B.J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle B.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RX Kanincker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a Genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP Berkeley *Drosophila* Genome Project;
RG Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacle B.J., Park S., Swirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC Q9VX08:CG6769; NbExp=1; IntAct=EBI-153770, EBI-128541;
CC Q9VFP7:CG9926; NbExp=1; IntAct=EBI-153770, EBI-154466;
CC Q87X3:1(1)G0136; NbExp=1; IntAct=EBI-153770, EBI-133004;
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL: AE003552; AAF50310.1; -; Genomic_DNA.
CC
CC IntAct; Q9VSV1; -;
DR FlyBase; EBN0035968; CG4484.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 2.
SQ SEQUENCE 599 AA; 66058 MW; C5381D334CFBF2EB CRC64;

Query Match 18.2%; Score 519.5; DB 2; Length 599;
Best Local Similarity 23.7%; Pred. No. 4.7e-31;
Matches 150; Conservative 100; Mismatches 201; Indels 183; Gaps 14;

QY 12 RHRKAQLLVNLLTFGLEVCVLAAGTYVPPPLLEVLVEEKEKFTWLVGICPVGLVCVPLL 71
DB 46 RKTREMPFLSAIAAIEAPYAAETSFVSPILLQIGVDHKHMSMTWGLSPGLFFMSPLL 105
QY 72 GSASDHWGRGRRRPFIFWALSIGLISLFLIP; - - - - -R 105
DB 106 GSISDRCKLRWGRRRPFIISLFGIMCGILIPYKDKLGLLDGAGTYAESALNFTSS 165
QY 106 AGWLAGLLC- - - - -PDPRLELA- - - - -LLILGVGLDFCGQVCFPTLEALLSLDFRDPDHC 157
DB 166 GGSVAALVSGEATTGPSASDYKFAVILITILGMVLLDFDADTCQTPARTYLLDMC-VPBEQ 224
QY 158 RQAYSVYAFMISLGGCLGVLPAIDWDTSAAPYLGTQBECLFGLTLFLTCVAATL- - 215
DB 225 PRAMTWFAFAGFGGTIGYAGIGVDWETTHISFGMGNPTVFTLVITIFAVCYLITVIT 284
QY 216 - - - - -LVAEEAALGP- - - - -KKNNIYIYIQTTLQELQWASDDPKRLEALQG 231
DB 285 FREIPLIEQDELLRPLSEQAIKKELKKNNIYIYIQTTLQELQWASDDPKRLEALQG 344
QY 232 LSAPSLSP- - - - -HCCPCRARLAFRNALGALLPRHLQLCRMPRLRL 275
DB 345 SYQNGYSPAVEKQKGSQDLETQSDYDAPVSLKAYLSIFI- - - - -MPYSMRMLA 393
QY 276 VAECLCSWMAIMTTLFTYTDVGEGLYQGVPRAPGTEARRHYDEGVGMGSLGLFLQCAIS 335
DB 394 LTNLFCWMGHVITCYLFTDFVGEAVFHGDDTAAPNSEALNLYBAGVRFGCWGAIVAFSC 453
QY 336 LVFSLVMDRUVORFGRVAVLASVAAPFV- - - - -AAGATCCLSHSVAVVTASALTGFTFSAL 392
DB 454 SYVLSVTYKLMKWFQKAVYISGMIVYIGMLVGLMPTKMWGLVVFSTSA- - - - -GILYGTI 510
QY 393 QILPYTLASLYHREKQVFLPKYRGDTGGASSEDLSMTSLFLPGPKPGAPFNGHVAGGSG 452
DB 511 FTVPFILVARYH-KNCFSIK- - - - -NG- - - - -NG- - - - -NG- - - - -NG- - - - -NG- 532

QY 453 LLPPPALCGASACDVSRVVVGEPTARVVP---GRGICLDLAILDSAFLLSQVAPSLF 509
 Db 533 -----EIVPLKQARGICTDVAIISSMVFIAQLIVSL 564
 QY 510 MGSIVQLSQSVTAYMYSAAGLGLVAIYATQVVF 543
 Db 565 VGPLVSMWDTTCALVYASTFLSLAATAAMFVLY 598

RESULT 11

Q4R136_TETNG
 ID Q4R136_TETNG PRELIMINARY; PRT; 675 AA.
 AC Q4R136;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Chromosome 8 SCAP15044, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG0034054001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasiuila C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Bieumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Ciraudo C., Duprat S., Brottier P., Coutanceau J.-P., Guzy J.,
 RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn W., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Scherzer E.S., Weissenbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; CAAE01015044; CAG11946.1; -; Genomic_DNA.
 DR NON_TER 675
 SQ SEQUENCE 675 AA; 4350FP19P4D3533B CRC64;

Query Match 17.2%; Score 491; DB 2; Length 675;
 Best Local Similarity 24.4%; Pred. No. 8.2e-29;
 Matches 165; Conservative 79; Mismatches 199; Indels 232; Gaps 17;
 QY 26 FGLEVLCAAGITVVPPLLVGVGVEEKFMVTMLVGLVGVPLVGLSADHWGRYGR 85
 Db 63 FGREFCYMETALVTPVLLQIGLPEQYSLTWFLSPILGLVFTVPVIGTASDRCVLWGR 122
 QY 86 RPFIALSLGILL--SLFLIPRAGWLAGLCL---PDRPLELALLILGVGLLDFCCQVCF 140
 Db 123 RPFIALCGALLGVALFL---NGSLIGLSVGRPGSQPTGLVTLVGLVVLDFSDAAAE 179
 QY 141 TPEALLSLDFRPDCHRCQAYSVAFMISLGGCLGYLLPAIDNWTALAPYLGTQECFL 200
 Db 180 GPIRAYLLDV-ADTERQDMALNTHAFSAGLGGVAGVMGLGLDWTGTALGRAFKSQBVLF 238

QY 201 GLTLFLITCV-----AATLL--VAEE- 220
 Db 239 LPASIIIFIISVILHLSFIEQPPVPTSQLKAABSGSSSOTSFRASISQLAPLLDAIEED 298
 QY 221 --AAL-----GPT-----EPAGLSAPLSLPHC----- 241
 Db 299 FSAAQONDCSELNGPTNLQPPDPVGHQOQTKAVNGASPGASSGHCNAVKGOTSTRFT 358
 QY 242 -----CPCRL-----AFRLGA 255
 Db 359 NHPSSTSASPRPHPTFFRQPSFTFSYGRVGRQFRRLRTAPSRPOPITTSRLNDLSE 418
 QY 256 LPLRLHQ-----LCCRMPTRLRLRFLVAELCSWMLMT 287
 Db 419 LPQRLDRRLQLSTSTLSSESSNLLTKCLLFLSSQMPKQLWRCLCHLLTWFSIMA 478
 QY 288 FTLPYTDFTVGEGLYQGVPRAPRPGTEARRHYDEGRVMSGLGLFLOCAISLVFLVMDRLVQ 347
 Db 479 EAVFYTDFMGQVIYHGDPTAPANSTDLQNVNRGVQMGVGLVYVYATAAVCSAILQKYLD 538
 QY 348 RF--GTRAVYLVASVAAPPAAGATCLSHSVAVVTASAALTGFTFSALOILPYTLASLYHR 405
 Db 539 NFDSLKIYIVTGLTGFSGAGTAFIAFPNVYVAVMWMISSMGVISMISICPYALLGOYHE 598
 QY 406 EKQVFLPKYRGDTGCGASSEDLSMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASA 465
 Db 599 IKEV-----C 603
 QY 466 CDVSVRVVVGTEARVVRGICLDLAILDSAFLLSQVAPSLFMSGISVOLSQSVTAYMV 525
 Db 604 SDTSI-----PANTR-----RGFIDCAILSCQVYSQILVASALGSDVDAVGSVRVIPA 653
 QY 526 SAAG---LGLVAIYF 537
 Db 654 VASGSGFLGLTACF 668
 RESULT 12
 S45A2_MOUSE
 ID S45A2_MOUSE STANDARD; PRT; 530 AA.
 AC P58355;
 DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
 DT 16-NOV-2001, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Membrane-associated transporter protein (AIM-1 protein) (Melanoma
 DE antigen AIM1) (Solute carrier family 45 member 2) (Underwhite
 DE protein).
 GN Name=SLC45A2; Synonyms=Aim1, Matp, uw;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=GDY; TISSUE=Eye, Kidney, and Uterus;
 RX MEDLINE=21372467; PubMed=11479596; DOI=10.1038/ng584;
 RA Fukunachi S., Shimada A., Shima A.;
 RT "Mutations in the gene encoding B, a novel transporter protein, reduce
 RT melanin content in medaka.";
 RL Nat. Genet. 28:381-385 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANTS UW-DBR ASN-153 AND PRO-435.
 RX MEDLINE=21473748; PubMed=11574907;
 RA Newton J.M., Cohen-Barak O., Hagiwara N., Gardner J.M., Davison M.T.,
 RA King R.A., Brilliant M.H.;
 RT "Mutations in the human orthologue of the mouse underwhite gene (uw)
 RT underlie a new form of oculocutaneous albinism, OCA4.";
 RL Am. J. Hum. Genet. 69:981-988 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Aweiler R., Aturaliya R.N., Bailey T.L.,
RA Baul M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Gatta G.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Taki K.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tammaja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
CC -I- FUNCTION: Melanocyte differentiation antigen. May transport
CC substances required for melanin biosynthesis (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By
CC similarity).
CC -I- TISSUE SPECIFICITY: Melanocytes, eyes, kidney and uterus.
CC -I- DISEASE: Defects in Slc45a2 are the cause of the uw-dbr phenotype
CC that results in loss of nearly all pigmentation in the homozygous
CC state.
CC -I- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -----
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CC -----
CC ENBL; AF360357; AAK81713.1; -; mRNA.
CC ENBL; AK029155; BAC26330.1; -; mRNA.
CC Ensembl; ENSMUSG000002243; Mus musculus.
CC MGI; MGI:2153040; Slc45a2.
CC GO; GO:0048066; P:pigmentation during development; IMP.
CC InterPro; IPR011701; MFS_1.
CC Pfam; PF07690; MFS_1; 1.
KW Albinism; Antigen; Disease mutation; Glycoprotein;
KW Melanin biosynthesis; Membrane; Sensory transduction; Transmembrane;
KW Vision.
FT CHAIN 1 530 Membrane-associated transporter protein.
FT /FtId=PRO_0000122518.
FT FT 1 45 Cytoplasmic (Potential).
FT TRANSMEM 46 66 1 (Potential).
FT TOPO_DOM 67 68 Extracellular (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT TOPO_DOM 90 105 Cytoplasmic (Potential).
FT TRANSMEM 106 126 3 (Potential).
FT TOPO_DOM 127 138 Extracellular (Potential).

FT TRANSMEM 139 159 4 (Potential).
FT TOPO_DOM 160 184 Cytoplasmic (Potential).
FT TRANSMEM 185 205 5 (Potential).
FT TOPO_DOM 206 216 Extracellular (Potential).
FT TRANSMEM 217 237 6 (Potential).
FT TOPO_DOM 238 318 Cytoplasmic (Potential).
FT TRANSMEM 319 339 7 (Potential).
FT TOPO_DOM 340 366 Extracellular (Potential).
FT TRANSMEM 367 387 8 (Potential).
FT TOPO_DOM 388 398 Cytoplasmic (Potential).
FT TRANSMEM 399 419 9 (Potential).
FT TOPO_DOM 420 425 Extracellular (Potential).
FT TRANSMEM 426 446 10 (Potential).
FT TOPO_DOM 447 477 Cytoplasmic (Potential).
FT TRANSMEM 478 498 Extracellular (Potential).
FT TOPO_DOM 499 504 12 (Potential).
FT TRANSMEM 505 525 12 (Potential).
FT TOPO_DOM 526 530 Cytoplasmic (Potential).
FT CARBOHYD 536 356 N-linked (GLCNAC...) (Potential).
FT VARIANT 153 153 D -> N (in UW-dbr).
FT VARIANT 435 435 S -> P (in UW-dbr).
SQ SEQUENCE 530 AA; 57961 MW; F4EEDAD07916D9FC CRC64;
Query Match 17.1%; Score 489.5; DB 1; Length 530;
Best Local Similarity 26.1%; Pred. No. 8.2e-29;
Matches 146; Conservative 85; Mismatches 228; Indels 101; Gaps 12;
QY 17 QLLVNLITFLGLEVCCLAIGIYVPLLEVGVEKFMVMVLGIGVPLGLVCVPLLSASD 76
Db 34 RLVMHSMAMFGREFCYAVAAAYVTPVLLSVGLPKSLYSNMVLLSPILGLLQPVGSASD 93
QY 77 HWRGVRGRRRPIWALSIGLLSLFLIPRAGMLAGLLCPDRP---LELALLILGVGLLD 133
Db 94 HCRARWGRRRPILTLAIVMLLGMALYNGDAVVSALVANPRQKLIWALSITMVGWVLPD 153
QY 134 FCGQVCFTPLEALLSDLFRDPDHCQAVSVYAFMISLGGCLGYLLPAIDWDTSALAPYL 193
Db 154 PSADFDIGPIKAYLPDVCVSHQDK-EKGLHYHALFTGFGGALGYILGAIDMVHLDLRLLG 212
QY 194 TQEECLFGLLTILFLTCVAATLLVAEEAAL--GPTEP-----AEGLSAPLSPHCCPC 244
Db 213 TEFQVNFSSALVILCFITHLCSIPAEPLRDAADPPSQDPPQSSLSASGMHEY---- 268
QY 245 RARLAFRNLGA-----LLPRLHQLCCMRPTLRRLFLVABLCSW 282
Db 269 GSIEKVKNGADTEQPVQEMKNKFGSQSQRTSMKSLRLALVNMPSHYRCLCVSHLIGW 328
QY 283 MALMTFTFLPYTDFVGEGLYQGVPRAPDPTGTEARRHHDGVRMGSLGLFLOCAISLPSLV 342
Db 329 TAPLSNMLPFTDFMGQIVVHGDPYGAHNSTEFLLYERGVGVCWGLCINSVFSSVSYFQ 388
QY 343 DRLVQRFGRTRAVYLASVAAPFAAGATCLSHSVAVVTAASAALTGFTFSALQILPYTLASL 402
Db 389 KAMVSYIGLUGLYFMGYLLFGLTGTFIGLFPNVYSTLVLCSMFGVMSSTLYTVFPNLIAE 448
QY 403 YHREKQVFLPKYRGDTGGASSEDLSMTSFLPGPKGAPPNGHVAGGSGLLPPPALCG 462
Db 449 YHREEE---KEKGQEA-----PGGPDNQR---GKGV-----DCA 477
QY 463 ASACDVSVRVVVGEPTEARVVPGRGICLDLALDSAFLLSQVAPSLFMGSIVOLSOVTA 522
Db 478 ALTCMVQL-----AQILVGGG-----LGLFLNMAGSVVV 506
QY 523 YMVSAAGLGLVAIYFATQVV 542
Db 507 VVITASVSLIGCCCFVALFV 526
RESULT 13
Q541S3_MOUSE
ID Q541S3_MOUSE PRELIMINARY; PRT; 530 AA.
AC Q541S3;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.

RX PubMed=14722913; DOI=10.1002/humu.10311;
RA Runderhagen U., Zuehlke C., Opitz S., Schwinger E.,
RA Kaemann-Kellner B.;
RT "Mutations in the MATP gene in five German patients affected by
RT oculocutaneous albinism type 4.";
RL Hum. Mutat. 23:106-110(2004).
RN [7].
RP VARIANTS LYS-272; LEU-374 AND LEU-507.
RX PubMed=1545243; DOI=10.1007/s00414-004-0490-z;
RA Yuasa I., Umetsu K., Watanabe G., Nakamura H., Endoh M., Irizawa Y.;
RT "MATP polymorphisms in Germans and Japanese: the L374F mutation as a
RT population marker for Caucasoids";
RL Int. J. Legal Med. 118:364-366(2004).
RN [8].
RP VARIANT OCA4 ASN-157.
RX PubMed=15656822; DOI=10.1111/j.1365-2133.2005.06403.x;
RA Suzuki T., Inagaki K., Fukui K., Obana A., Lee S.-T., Tomita Y.;
RT "A Korean case of oculocutaneous albinism type IV caused by a D157N
RT mutation in the MATP gene.";
RL Br. J. Dermatol. 152:174-175(2005).
CC -!- FUNCTION: Melanocyte differentiation antigen. May transport
CC substances required for melanin biosynthesis (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=AIM-1a;
CC IsoId=Q9UMX9-1; Sequence=Displayed;
CC Name=AIM-1b;
CC IsoId=Q9UMX9-2; Sequence=VSP_006297, VSP_006298, VSP_006299;
CC Name=AIM-1c;
CC IsoId=Q9UMX9-3; Sequence=VSP_006296;
CC -!- TISSUE SPECIFICITY: Expressed in most melanoma cell lines and
CC melanocytes.
CC -!- DISEASE: Defects in SLC45A2 are the cause of oculocutaneous
CC albinism type 4 (OCA4) [MIM:606574]. OCA4 is an autosomal
CC recessive disorder of pigmentation characterized by reduced
CC biosynthesis of melanin in the skin, hair and eyes. It leads to
CC reduced visual acuity.
CC -!- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 188.
CC -!- CAUTION: The described alternatively spliced isoforms are inferred
CC using information from ESTs.
CC -!- DATABASE: NAME=Mutations of the MATP gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/matpmt.htm".
CC -----
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CC -----
DR EMBL: AF172849; AAD51812.1; -; mRNA.
DR EMBL: BC003597; AA03597.1; ALT_FRAME; mRNA.
DR GenBank: U000001641.75; Homo sapiens.
DR HGNC: HGNC:16472; SLC45A2.
DR MIM: 606574; gene.
DR MIM: 606574; phenotype.
KW Albinism; Alternative splicing; Antigen; Disease mutation;
KW Glycoprotein; Melanin biosynthesis; Membrane; Polymorphism;
KW Sensory transduction; Transmembrane; Vision.
FT CHAIN 1 530 Membrane-associated transporter protein.
FT FTId=PRO_0000122517.
FT FT TOPO_DOM 1 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 1 (Potential).
FT TOPO_DOM 68 68 Extracellular (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT TOPO_DOM 90 110 Cytoplasmic (Potential).
FT TRANSMEM 111 131 3 (Potential).
FT TOPO_DOM 132 138 Extracellular (Potential).
FT TRANSMEM 139 159 4 (Potential).
FT TOPO_DOM 160 184 Cytoplasmic (Potential).

FT TRANSMEM 185 205 5 (Potential).
FT TOPO_DOM 206 216 Extracellular (Potential).
FT TRANSMEM 217 237 6 (Potential).
FT TOPO_DOM 238 318 Cytoplasmic (Potential).
FT TRANSMEM 319 339 7 (Potential).
FT TOPO_DOM 340 366 Extracellular (Potential).
FT TRANSMEM 367 387 8 (Potential).
FT TOPO_DOM 388 398 Cytoplasmic (Potential).
FT TRANSMEM 399 419 9 (Potential).
FT TOPO_DOM 420 425 Extracellular (Potential).
FT TRANSMEM 426 446 10 (Potential).
FT TOPO_DOM 447 477 Cytoplasmic (Potential).
FT TRANSMEM 478 498 11 (Potential).
FT TOPO_DOM 499 504 Extracellular (Potential).
FT TRANSMEM 505 525 12 (Potential).
FT TOPO_DOM 526 530 Cytoplasmic (Potential).
FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 129 187 Missing (in isoform AIM-1c).
FT VARSPLIC 188 295 Missing (in isoform AIM-1b).
FT VARSPLIC 386 406 YFQKVLVSITGKGLYFTGYL -> CKSFSLRLMSKSPWS
FT STTWI (in isoform AIM-1b).
FT FTId=VSP_006298.
FT VARSPLIC 407 530 Missing (in isoform AIM-1b).
FT VARIANT 58 58 P -> A (in OCA4).
FT VARIANT 58 58 P -> S (in OCA4).
FT VARIANT 157 157 D -> N (in OCA4).
FT VARIANT 188 188 G -> V (in OCA4).
FT VARIANT 202 202 W -> C (in OCA4).
FT VARIANT 221 221 Missing (in OCA4).
FT VARIANT 272 272 E -> K.
FT VARIANT 317 317 Y -> C (in OCA4).
FT VARIANT 361 361 L -> P (in OCA4).
FT VARIANT 374 374 F -> L (common polymorphism;
FT dbSNP:168991982).
FT VARIANT 477 477 A -> T (in OCA4).
FT VARIANT 486 486 A -> V (in OCA4).
FT VARIANT 500 500 T -> P.
FT VARIANT 507 507 V -> L.
FT VARIANT 530 530 AA; 58302 MW; F14A4BACA8FF31B CRC64;
FT SQ SEQUENCE 530 AA; 58302 MW; F14A4BACA8FF31B CRC64;
FT SQ
Query Match 17.1%; Score 488.5; DB 1; Length 530;
Best Local Similarity 26.4%; Pred. No. 9.8e-29;
Matches 150; Conservative 78; Mismatches 233; Indels 107; Gaps 12;
QY 8 SLLLRKAQLLLVNLTFGLBVCCLAAAGITYVPPLLEVGVEEKFTMTWLGIPVLGLVC 67
DB 33 SLLIWHSMAM-----FGREFCVAEAYVTPVLLSVGLPSSLSYIVWFLSPILGFL 84
QY 68 VFLGASADHWGRYGRPPFTWALSGLILLSLFIIPRAGWAGLICPPDR---PLELAL 124
DB 85 QPVGASADHCRSRGRRRPYILTGLVNLVGLMALVNGATVVAALIANPRKLVWISV 144
QY 125 LILGVGLDFCCQVCFPLEALLSDFPRDPHCRQAYSVYAFMISLGGCIGYLLPAIDWD 184
DB 145 TMIGVVLDFDAADFIDGPIKAYLFDVCSHODK-EKGLHYHALFTGFGGALGYLLGIDWA 203

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